



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/346,794	07/02/1999	TERRY P. SNUTCH	NMEDP001-2	2888

25225 7590 03/13/2007
MORRISON & FOERSTER LLP
12531 HIGH BLUFF DRIVE
SUITE 100
SAN DIEGO, CA 92130-2040

EXAMINER

BASI, NIRMAL SINGH

ART UNIT	PAPER NUMBER
----------	--------------

1646

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	03/13/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary

Application No.

09/346,794

Applicant(s)

SNUTCH ET AL.

Examiner

Nirmal S. Basi

Art Unit

1646

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 05 October 2006.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 28-31, 37 and 40 is/are pending in the application.
- 4a) Of the above claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 28-31, 37 and 40 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. _____.
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO/SB/08)
Paper No(s)/Mail Date 11/11/07
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) ☐ Notice of Informal Patent Application
- 6) ☐ Other: _____

DETAILED ACTION

1. The Board of patent Appeals and Interferences reversed Examiners rejection for lack of utility in the decision dated 11/22/06. The Board further indicated that the effective filing date of the claims appears to be July 2, 1999 since the parent application 09/030482 does not disclose the full-length cDNA, SEQ ID NO:23 (7450 nucleotides long), encoding the rat α_{1G} subunit of a t-type calcium channel. The '482 application provide partial sequences. Therefore, upon further review the priority is not granted to the '482 parent application. The Board decision states, page 10, "Therefore, the claims on appeal do not appear to be supported by the earlier application in the manner required by 35 U.S.C. § 112, first paragraph. Lacking such support, the present claims would not be entitled to the benefit of priority under 35 U.S.C. § 120 based on the earlier-filed application; the effective filing date of the claims appears to be July 2, 1999." Therefore, the present claims are not be entitled to the benefit of priority under 35 U.S.C. § 120 based on the earlier-filed application; the effective filing date of the claims is July 2, 1999.

2. Board of patent Appeals and Interferences decision dated 11/22/06 also states, "On return of this application, however, we recommend that the examiner consider the differences between the method disclosed by Perez-Reyes and the methods defined by the pending claims. If the examiner believes that the differences are such that the claimed methods would have been obvious in view of the prior art method, a rejection

Art Unit: 1646

based on 35 U.S.C. § 103 should be entered. If a new rejection is made, of course, Appellants must be given an appropriate opportunity to respond." The examiner has determined the claimed methods are obvious in view of the prior art, a rejection based on 35 U.S.C. § 103 is entered. Appellants are given an appropriate opportunity to respond as required by the Board.

Claim Rejections - 35 USC § 103

3. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

The factual inquiries set forth in *Graham v. John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was

Art Unit: 1646

not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 28-31, 37 and 40 are rejected under 35 U.S.C. 103(a) as being unpatentable over Perez-Reyes (WO 99/29847) or Perez-Reyes (Nature, Vol. 391, pages 900,1998) in view of Harpold et al (US Patent 5,429,921) as it applies to claims 28, 29, 31, 37 and 40, and in view of Brown et al (US Patent 5,688,938) or Okun et al (US Patent 5,804,36) as it applies to claims 28 and 30 .

The Boards analysis of Perez-Reyes (WO 99/29847) was:

"The amino acid sequences of full-length T-type channels, and the sequences of suitable coding nucleic acids..., at SEQ ID NOs:1-8 (α 1G sequences)." Page 6, lines 5-7. Perez-Reyes indicates that SEQ ID NO:5 is derived from rat ("Rattus sp."). See page 37. Amino acids 33 to 2254 of the sequence encoded by Perez-Reyes' SEQ ID NO:5 appear to be virtually identical to amino acids 65 to 2287 of the sequence encoded by the present application's SEQ ID NO:23.

Perez-Reyes discloses a method of identifying a drug which affects T-type calcium channels. The method involves first expressing a T-type calcium channel in a cell to produce an active channel The cell expressing the channel is then exposed to a solution containing a putative drug for interfering with the channel. Thereafter, the presence or absence of calcium flux in response to a change in membrane potential is assayed. Page 11, lines 7-12.

Perez-Reyes also includes a working example showing that "mibefradil almost completely abolished T-type current in cells expressing α 1G." Page 18. The example is said to "demonstrate[] that a cloned T-type calcium channel can be used for identifying a drug which affects T-type calcium channels." Id. Thus,

Art Unit: 1646

Perez-Reyes reasonably appears to disclose a method of identifying drugs that affect T-type calcium channels using cells expressing a rat $\alpha 1G$ calcium channel subunit.

However, Perez-Reyes does not reasonably appear to disclose the specific methods defined by claims 28 and 31, the only independent claims remaining in the present application. Claim 28 requires contacting a recombinant cell expressing an $\alpha 1G$ subunit "with a known agonist of [a] T-type calcium channel," while claim 31 requires determining binding of a test compound to a cell expressing an $\alpha 1G$ subunit "by observing competitive binding with a known agonist or antagonist of [a T-type calcium] channel.

Perez-Reyes does not disclose either of these limitations and therefore does not appear to anticipate the presently pending claims."

The sequence comparisons of the T-type voltage gated calcium channels disclosed by Perez-Reyes (WO 99/29847) are provided as Appendix A, below. Perez-Reyes (WO 99/29847) discloses nucleic acids (AAX83485-AAX83488) encoding T-type voltage gated calcium channel $\alpha 1G$ polypeptides. The nucleic acids all have greater than 88% query match and greater than 99% best local similarity with the nucleic acid SEQ ID NO:23 of instant application. Perez-Reyes (WO 99/29847) further discloses polypeptides (AAY14590-AAY14593) comprising T-type voltage gated calcium channel $\alpha 1G$ polypeptide. The polypeptides all have greater than 96% query match and greater than 99% best local similarity with the polypeptide of SEQ ID NO:24 of instant application. The nucleic acids (AAX83485-AAX83488) disclosed by Perez-Reyes will

Art Unit: 1646

also hybridize under stringent hybridization conditions to the nucleic acid comprising the sequence disclosed in SEQ ID NO:23, absent evidence to the contrary.

Perez-Reyes (Nature, Vol. 391, 1998) discloses a nucleic acid (Accession no. AF027984) which has 99.6% query match and 99.8% best local similarity to SEQ ID NO:23 of instant application (see Appendix B for sequence comparison). Also disclosed is a polypeptide (Accession number T09053) which has 96.9% and 99.7% sequence identity to SEQ ID NO:24 (see Appendix for sequence comparison).

Harpold (US Patent 5,429,921) discloses assays for agonists and antagonists of calcium channels. Harpold discloses (see columns 9-12, claims, specifically claims 1 and 7) methods to identify an agonists or antagonist of a calcium channels which comprise: a) contacting a cell recombinant expressing a heterologous calcium channel with an agonist of said T-type calcium channel; b) contacting said cell with a compound to be tested; and c) determining the ability of said compound for activity as an antagonist (i.e. diminish the activation of subunit by said agonist) or activity as an agonist. The use of controls, which are required to determine functional activity of the calcium channel when testing agonists or antagonists, is disclosed in column 11 (third paragraph).

Column 7 states,

"In an especially preferred embodiment, the invention entails a eukaryotic cell comprising a recombinant calcium channel consisting essentially of human subunits, said recombinant channel being **capable of binding agonist or antagonist** compounds and/or passing calcium channel selective ions. In another of its aspects the invention employs a eukaryotic cell which expresses on its surface functional heterologous calcium channels of the invention in methods for identifying agonists and antagonists of

Art Unit: 1646

calcium channel activity in humans and/or assessing the contribution of the various calcium channel subunits to the transport and regulation of calcium ions."

Column 10 discloses that a method of the invention that entails a ligand binding assay for testing a compound for capacity to specifically bind to a calcium channel.

Column 16 discloses:

"The capacity of a test compound to bind to membranes comprising heterologous calcium channels or subunits thereof may be determined by any appropriate **competitive binding analysis** (e.g., Scatchard plots), wherein the binding capacity of such membranes is determined in the presence and absence of one or more concentrations of a compound having known affinity for the calcium channel. As a control, these results may be compared to an identically treated membrane preparation from host cells which were not transfected with one or more subunit-encoding nucleic acids (i.e., a negative control).

Okun et al (US Patent 5,804,436) discloses the use of fluorescent dyes in identifying agonists and antagonists of calcium channels. Okun states:

"A development of intracellular fluorescent calcium indicators (Grynkiewicz et al., 1985, is incorporated herein by reference) made it possible for intracellular concentration of free calcium to be measured directly in the living cell. Thus the ability to register changes in intracellular calcium concentration provide the means for monitoring effects of different compounds useful in treating various diseases, whose action is thought to be a result of an interaction with membrane receptors and ion channels."

"A variety of effects caused by the compounds to be screened may be detected and quantitatively characterized according to the present invention. Preferably, these effects include but are not limited to changes in intracellular concentration of ionized calcium, cAMP or pH, transmembrane potential and other physiological and biochemical characteristics of living cell which can be measured by a variety of conventional means, for example using specific fluorescent luminescent or color developing dyes."

"The present invention also includes methods of screening for agonist or antagonist activity of drugs."

"The cells grown in accordance with the preferred embodiments described above, are mixed with an appropriate fluorescent dye for example FURA-2AM for measurements of concentrations of intracellular calcium or BCECF-AM for measurements of intracellular pH, and are incubated in the appropriate conditions to allow the dye to penetrate into the cell. The cells loaded with a dye are supplied to the apparatus. In the apparatus, the cells are successively mixed with a solutions of the compounds to be tested."

Brown (US Patent 5,688,938) discloses the use of fluorescent dyes in identifying agonists and antagonists of calcium channels.

Brown states:

"Changes in Ca^{2+} are readily monitored and quantitated using fluorimetric indicators such as fura-2 or indo-1 (Molecular Probes, Eugene, Oreg.). Measurement of Ca^{2+} provides an assay to assess the ability of molecules to act as agonists or antagonists at the calcium receptor", (see Background of the Invention)."

It would have been prima facie obvious to a person of ordinary skill in the art at the time the invention was made to use the nucleic acid encoding T-type voltage gated calcium channel α_{1G} polypeptides disclosed by Perez-Reyes in the methods for identifying agonists and antagonists for the calcium channels as disclosed by Harpold et al.. The activation could be measured by many techniques well known in the art, for example, using fluorescent dyes as disclosed by Brown and Okun, or measuring the current through the calcium channel as disclosed by Perez-Reyes and Harpold. The ordinary artisan would have been motivated to use the T-type voltage gated calcium channel α_{1G} polypeptides disclosed by Perez-Reyes in the methods of Harpold et al. to identifying agonists and antagonists for the newly discovered T-type voltage gated calcium channel. Perez-Reyes (WO 99/29847) envisions characterizing their newly discovered channel protein, and on page 3 states, "The present invention is useful for exploring the electrophysiological pharmacology of the T-type calcium current. Such knowledge can lead to the development for potentiating or attenuating T-type calcium channels". Page 18 states, when referring to Example 6, "This example demonstrates that a cloned T-Type calcium channel can be used for identifying a drug which affects T-type calcium channels". Newly discovered channel proteins and receptors are routinely assayed for agonists and antagonists using standard methods well accepted in the art. These methods can comprise ligand binding studies or activity studies using well known biochemical techniques and kinetic analysis. The ordinary artisan would have expected success at using the method of Harpold by incorporating the T-type calcium channel of

Art Unit: 1646

Perez Reyes to identify agonists and antagonists because many channel proteins have been characterized by their sensitivity to agonists and antagonists (Harpold column 2).

For the reason given above the invention of claims 28-31, 37 and 40 is prima facie obvious.

Applicants can overcome examiners rejection by limiting the methods to identifying antagonists of the T-type calcium channel encoded by the nucleic acid of SEQ ID NO:23 or prescreening compounds as agonists or antagonists of the T-type calcium channel encoded by the nucleic acid of SEQ ID NO:23.

Claim Objections

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Upon further review claims 37 and 40 are objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form.

Claim 37 states, when referring to the method of claim 28, "wherein the nucleic acid comprises SEQ ID NO:23." The nucleic acid of claim 28 already comprises SEQ ID NO:23 and claim 37 fails to further limit the nucleic acid.

Art Unit: 1646

Claim 40 states, when referring to the method of claim 31, "wherein the nucleic acid comprises SEQ ID NO:23." The nucleic acid of claim 31 already comprises SEQ ID NO:23 and claim 40 fails to further limit the nucleic acid.

5. No claim is allowed.

Advisory

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Nirmal S. Basi whose telephone number is 571-272-0868. The examiner can normally be reached on 9:00 AM-5:30 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Nickol can be reached on 571-272-0835. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

N. S. Basi
Art Unit 1646

NSB

Gary Nickol

GARY B. NICKOL, PH.D.
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Art Unit: 1646

Appendix A

Database search of nucleic acid and polypeptide sequence with the greatest identity to SEQ ID NO :23 and SEQ ID NO:24 are provided below. A comparison of the sequences disclosed by Perez-Reyes, W. (WO 99/29847) that have greatest identity with SEQ ID NO :23 and SEQ ID NO:24 are provided in detail.

GenCore version 6.2
Copyright (c) 1993 - 2007 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 9, 2007, 10:25:02 ; Search time 4421 Seconds
(without alignments)
12638.697 Million cell updates/sec

Title: US-09-346-794-23
Perfect score: 7540
Sequence: 1 ccgtctctggcgcgagcg.....acgtttgtgcagaatctcta 7540

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*

Art Unit: 1646

12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*
 16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	7540	100.0	7540	5	AAF31677	Aaf31677 Rat alpha
2	6956.4	92.3	7286	3	AAZ52309	Aaz52309 Rat pancr
3	6910.4	91.6	6942	13	ADS16295	Ads16295 Rat volta
4	6730.4	89.3	6762	2	AAX83485	Aax83485 Rat T-typ
5	6678.4	88.6	6741	2	AAX83488	Aax83488 Rat T-typ
6	6665	88.4	6795	2	AAX83486	Aax83486 Rat T-typ
7	6661.6	88.4	6816	2	AAX83487	Aax83487 Rat T-typ
8	5810.6	77.1	7741	4	AAD04756	Aad04756 Human T-t
9	5758.4	76.4	7520	14	AEC95681	Aec95681 Calcium c
10	5758.4	76.4	7520	15	AEI99684	Aei99684 Human CCA
11	5497.4	72.9	6750	2	AAX83481	Aax83481 Human T-t
12	5448.2	72.3	8002	4	AAH98402	Aah98402 Human EST
13	5447	72.2	6729	2	AAX83484	Aax83484 Human T-t
14	5432	72.0	6783	2	AAX83482	Aax83482 Human T-t
15	5431.8	72.0	6804	2	AAX83483	Aax83483 Human T-t
16	5431.6	72.0	6807	14	AEE17868	Aee17868 Human cDN
17	5427.2	72.0	6892	5	AAF31684	Aaf31684 Human alp
18	5167.4	68.5	7648	13	ADQ89063	Adq89063 Human uro
19	5167.4	68.5	7648	13	ADS16298	Ads16298 Human vol
20	3891.6	51.6	5337	14	AEC95682	Aec95682 Calcium c
21	3891.6	51.6	5337	15	AEI99685	Aei99685 Human CCA
22	3195	42.4	3993	4	AAS01624	Aas01624 Human T-t
23	3195	42.4	3993	15	AEK52292	Aek52292 Human T-t
24	2363.8	31.4	7277	14	AEC05418	Aec05418 Rat T-typ
25	2363.8	31.4	7426	14	AEC05414	Aec05414 Rat T-typ
26	2363.8	31.4	7432	14	AEC05416	Aec05416 Rat T-typ
27	2351	31.2	7898	2	AAX59080	Aax59080 Human act
28	2351	31.2	7898	8	ABZ58365	Abz58365 Human T-t
29	2349.8	31.2	8447	5	AAF31678	Aaf31678 Rat alpha
30	2348.4	31.1	7898	2	AAX59081	Aax59081 Human act
31	2341.8	31.1	7062	14	AEB12303	Aeb12303 Human T-t
32	2335.8	31.0	7895	14	AEC95664	Aec95664 Calcium c
33	2335.8	31.0	7895	15	AEI99667	Aei99667 Human CCA
34	2291	30.4	6132	2	AAX83489	Aax83489 Human T-t
35	2271	30.1	6114	2	AAX83490	Aax83490 Human T-t
36	1890.8	25.1	6990	13	ADS16296	Ads16296 Human vol
37	1890.8	25.1	6990	14	AEH10223	Aeh10223 Voltage-d
38	1812.2	24.0	2212	5	AAF31681	Aaf31681 Human alp
39	1798	23.8	5562	15	AEF53253	Aef53253 Human CAC
40	1798	23.8	6745	14	ADZ58491	Adz58491 Human alp
41	1796.8	23.8	6816	6	AAS16826	Aas16826 Human T-t
42	1796.8	23.8	6816	8	ABX93560	Abx93560 Human cDN
43	1796.8	23.8	6816	12	ADH69264	Adh69264 Human TCC
44	1796.8	23.8	6855	6	AAS16827	Aas16827 Human T-t
45	1796.8	23.8	6855	8	ABX93561	Abx93561 Human cDN

Art Unit: 1646

RESULT 4

AAX83485

ID AAX83485 standard; cDNA; 6762 BP.

XX

AC AAX83485;

XX

DT 07-DEC-1999 (first entry)

XX

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1a) cDNA.

XX

KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

XX

OS Rattus sp.

XX

PN WO9929847-A1.

XX

PD 17-JUN-1999.

XX

PF 30-OCT-1998; 98WO-US023161.

XX

PR 05-DEC-1997; 97US-00985809.

XX

PA (LOYO) UNIV LOYOLA CHICAGO.

XX

PI Perez-Reyes E, Cribbs LL;

XX

DR WPI; 1999-394972/33.

DR P-PSDB; AAY14590.

XX

PT New T-type voltage-gated calcium channels.

XX

PS Disclosure; Page 67-76; 138pp; English.

XX

CC This sequence represents the coding region for a rat T-type voltage-gated
CC calcium (Ca) channel alpha-1-G designated rCavT1a. Voltage gated channels
CC are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AAX83481-

Query Match 89.3%; Score 6730.4; DB 2; Length 6762;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6749; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

Qy	483	ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGTCGGGACAGCCCCGTAGCTTTCACG	542
Db	1	ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTTCACG	60
Qy	543	CAGCTCAACGACCTGTCCGGGGCCGGGGGC - -GGCAGGGGGCCGGGTTCGACGAAAAGGAC	600
Db	61	CAGCTCAACGACCTGTCCGGGGCCGGGGGC - -GGCAGGGGGCCGGGTTCGACGAAAAGGAC	120
Qy	601	CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT	660
Db	121	CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT	180
Qy	661	TTCTTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC	720
Db	181	TTCTTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC	240
Qy	721	CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG	780
Db	241	CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG	300
Qy	781	TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC	840
Db	301	TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC	360
Qy	841	GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC	900
Db	361	GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC	420
Qy	901	ATCTTTGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTTCATTGTC	960
Db	421	ATCTTTGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTTCATTGTC	480
Qy	961	ATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTGAGCTTCTCCGAGTCAGG	1020
Db	481	ATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTGAGCTTCTCCGAGTCAGG	540
Qy	1021	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCGAGCATGCGCATTCTC	1080
Db	541	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCGAGCATGCGCATTCTC	600
Qy	1081	GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCTGCTGCTCTGTTTCTTC	1140
Db	601	GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCTGCTGCTCTGTTTCTTC	660
Qy	1141	GTCTTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG	1200

Art Unit: 1646

Db 661 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 720

Qy 1201 TGCTTCCTCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 1260
|||||

Db 721 TGCTTCCTCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 780

Qy 1261 ACAGAGAATGAGGACGAGAGCCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA 1320
|||||

Db 781 ACAGAGAATGAGGACGAGAGCCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA 840

Qy 1321 TCCTGCAGGAGTGTGCCCACTGCGTGGGGAAGGCGGTGGTGGCCACCCTGCAGTCTG 1380
|||||

Db 841 TCCTGCAGGAGTGTGCCCACTGCGTGGGGAAGGCGGTGGTGGCCACCCTGCAGTCTG 900

Qy 1381 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 1440
|||||

Db 901 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 960

Qy 1441 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1500
|||||

Db 961 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1020

Qy 1501 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1560
|||||

Db 1021 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1080

Qy 1561 TACTTCGTAATGGACGCTCACTCCTTCTACAACTTCATCTACTTCATTCTTCTCATCATC 1620
|||||

Db 1081 TACTTCGTAATGGACGCTCACTCCTTCTACAACTTCATCTACTTCATTCTTCTCATCATC 1140

Qy 1621 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1680
|||||

Db 1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1200

Qy 1681 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGGTACGATTCTGTCCAATGCT 1740
|||||

Db 1201 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGGTACGATTCTGTCCAATGCT 1260

Qy 1741 AGCACCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1800
|||||

Db 1261 AGCACCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1320

Qy 1801 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1860
|||||

Db 1321 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1380

Qy 1861 CGGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCAGTGGC 1920
|||||

Db 1381 CGGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCAGTGGC 1440

Qy 1921 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1980
|||||

Db 1441 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1500

Qy 1981 CACCATCACCCTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG 2040
|||||

Db 1501 CACCATCACCCTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG 1560

Qy 2041 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGTACCACCACCCTCTACACCC 2100
|||||

Art Unit: 1646

Db 1561 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACACCC 1620

Qy 2101 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 2160
|||||

Db 1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 1680

Qy 2161 TGCCACTTGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCT 2220
|||||

Db 1681 TGCCACTTGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCT 1740

Qy 2221 GGTTAGGACTGTGGGTAGTGGGAAGGTGTACCCACTGTGCATACCAGCCCTCCACCAGAG 2280
|||||

Db 1741 GGTTAGGACTGTGGGTAGTGGGAAGGTGTACCCACTGTGCATACCAGCCCTCCACCAGAG 1800

Qy 2281 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACC 2340
|||||

Db 1801 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACC 1860

Qy 2341 AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 2400
|||||

Db 1861 AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 1920

Qy 2401 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGA 2460
|||||

Db 1921 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGA 1980

Qy 2461 GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCCGACAGGAGCAGGAGAGCCAGAGTCC 2520
|||||

Db 1981 GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCCGACAGGAGCAGGAGAGCCAGAGTCC 2040

Qy 2521 GCTGACCATGTGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT 2580
|||||

Db 2041 GCTGACCATGTGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT 2100

Qy 2581 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGACAGCGAGCCTGGGCCCAGAT 2640
|||||

Db 2101 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGACAGCGAGCCTGGGCCCAGAT 2160

Qy 2641 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2700
|||||

Db 2161 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2220

Qy 2701 GTAGATAGCAAATACTTTGGCCGGGAATCATGATCGCCATCCTGGTCAATACTCAGC 2760
|||||

Db 2221 GTAGATAGCAAATACTTTGGCCGGGAATCATGATCGCCATCCTGGTCAATACTCAGC 2280

Qy 2761 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTACCAACGCCCTGGAAATCAGCAAC 2820
|||||

Db 2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTACCAACGCCCTGGAAATCAGCAAC 2340

Qy 2821 ATCGTCTTCACCAGCCTCTTCGCCTTGAGATGTGCTGAAACTGCTTGTCTACGGTCCC 2880
|||||

Db 2341 ATCGTCTTCACCAGCCTCTTCGCCTTGAGATGTGCTGAAACTGCTTGTCTACGGTCCC 2400

Qy 2881 TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTGCTTGTGGTTCATCAGTGTG 2940
|||||

Db 2401 TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTGCTTGTGGTTCATCAGTGTG 2460

Qy 2941 TGGGAGATTGTGGGCCAGCAGGGAGGTGGCTGTGGTGTGCGGACCTTCCGCCTGATG 3000
|||||

Art Unit: 1646

Db 2461 TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCGTGATG 2520

Qy 3001 CGGGTGCTGAAGCTGGTGCGCTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG 3060
|||||

Db 2521 CGGGTGCTGAAGCTGGTGCGCTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG 2580

Qy 3061 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 3120
|||||

Db 2581 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 2640

Qy 3121 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG 3180
|||||

Db 2641 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG 2700

Qy 3181 TTGCCAGACCGGAAGAATTTGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 3240
|||||

Db 2701 TTGCCAGACCGGAAGAATTTGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 2760

Qy 3241 CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG 3300
|||||

Db 2761 CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG 2820

Qy 3301 GCTGCTCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 3360
|||||

Db 2821 GCTGCTCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 2880

Qy 3361 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 3420
|||||

Db 2881 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 2940

Qy 3421 CCTGATTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3480
|||||

Db 2941 CCTGATTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3000

Qy 3481 GTGGCTTTGGGAGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3540
|||||

Db 3001 GTGGCTTTGGGAGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3060

Qy 3541 ACGGCTGCGACACCAATGTACACCCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3600
|||||

Db 3061 ACGGCTGCGACACCAATGTACACCCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3120

Qy 3601 GGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3660
|||||

Db 3121 GGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3180

Qy 3661 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3720
|||||

Db 3181 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3240

Qy 3721 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCAGCCTAAAGCGG 3780
|||||

Db 3241 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCAGCCTAAAGCGG 3300

Qy 3781 AGGAGCCCGAGCGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3840
|||||

Db 3301 AGGAGCCCGAGCGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3360

Qy 3841 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3900
|||||

Art Unit: 1646

Db 3361 GAGGAGGAAAAGTTCAGAAGAGGACCGGGCCAGCCAGCAGGCAGTGACCATCGCCACAGG 3420

Qy 3901 GGTTCCCTTGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3960
|||||

Db 3421 GGTTCCCTTGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3480

Qy 3961 GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 4020
|||||

Db 3481 GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 3540

Qy 4021 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCCAACTGGATGGG 4080
|||||

Db 3541 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCCAACTGGATGGG 3600

Qy 4081 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTGAGA 4140
|||||

Db 3601 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTGAGA 3660

Qy 4141 TCCCGGCTTCTGCTGTGCGCGAGAGCGAGATTCTGGTTCGGCCTATATCTTTCTCTCT 4200
|||||

Db 3661 TCCCGGCTTCTGCTGTGCGCGAGAGCGAGATTCTGGTTCGGCCTATATCTTTCTCTCT 3720

Qy 4201 CAGTCAAGGTTTCGTCTCCTGTGTACCGGATCATCACCACAAAGATGTTTGACCATGTG 4260
|||||

Db 3721 CAGTCAAGGTTTCGTCTCCTGTGTACCGGATCATCACCACAAAGATGTTTGACCATGTG 3780

Qy 4261 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 4320
|||||

Db 3781 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 3840

Qy 4321 CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACCTACATCTTCACGGCAGTCTTT 4380
|||||

Db 3841 CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACCTACATCTTCACGGCAGTCTTT 3900

Qy 4381 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 4440
|||||

Db 3901 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 3960

Qy 4441 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTGATCGACATC 4500
|||||

Db 3961 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTGATCGACATC 4020

Qy 4501 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4560
|||||

Db 4021 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4080

Qy 4561 CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG 4620
|||||

Db 4081 CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG 4140

Qy 4621 GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC 4680
|||||

Db 4141 GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC 4200

Qy 4681 TTCTTCATCATTTTTTGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT 4740
|||||

Db 4201 TTCTTCATCATTTTTTGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT 4260

Qy 4741 CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA 4800
|||||

Art Unit: 1646

Db 4261 CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA 4320

Qy 4801 TGGGTCCGGCACAAGTACAACCTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG 4860
|||||

Db 4321 TGGGTCCGGCACAAGTACAACCTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG 4380

Qy 4861 CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG 4920
|||||

Db 4381 CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG 4440

Qy 4921 GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC 4980
|||||

Db 4441 GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC 4500

Qy 4981 CTCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTCCAT 5040
|||||

Db 4501 CTCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTCCAT 4560

Qy 5041 AAGTGCAGACAGCACCAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG 5100
|||||

Db 4561 AAGTGCAGACAGCACCAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG 4620

Qy 5101 AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGAAGCCAGTGCAAGCCC 5160
|||||

Db 4621 AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGAAGCCAGTGCAAGCCC 4680

Qy 5161 TACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTAC 5220
|||||

Db 4681 TACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTAC 4740

Qy 5221 CTGGACCTCTTCATCACTGGTGTGTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACAT 5280
|||||

Db 4741 CTGGACCTCTTCATCACTGGTGTGTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACAT 4800

Qy 5281 TACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTC 5340
|||||

Db 4801 TACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTC 4860

Qy 5341 ATCTTTGTCTTTGAGTCAGTTTTCAAACCTGTGGCCTTTGCGTTCCGCCGTTTCTTCCAG 5400
|||||

Db 4861 ATCTTTGTCTTTGAGTCAGTTTTCAAACCTGTGGCCTTTGCGTTCCGCCGTTTCTTCCAG 4920

Qy 5401 GACAGGTGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTG 5460
|||||

Db 4921 GACAGGTGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTG 4980

Qy 5461 GAGGAGATTGAGGTCAATCTGTGCTGCCCATCAACCCACCATCATCCGTATCATGAGG 5520
|||||

Db 4981 GAGGAGATTGAGGTCAATCTGTGCTGCCCATCAACCCACCATCATCCGTATCATGAGG 5040

Qy 5521 GTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTG 5580
|||||

Db 5041 GTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTG 5100

Qy 5581 CTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTA 5640
|||||

Db 5101 CTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTA 5160

Qy 5641 TTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAG 5700
|||||

Art Unit: 1646

Db 5161 TTGTTTTTCATCTTTGCAGCTCTGGGCGTGAGCTCTTTGGAGACCTGGAGTGTGATGAG 5220

Qy 5701 ACACACCCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACCTTGGTATGGCCTTT 5760
|||||

Db 5221 ACACACCCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACCTTGGTATGGCCTTT 5280

Qy 5761 CTGACCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACCCTTCC 5820
|||||

Db 5281 CTGACCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACACCCTC 5340

Qy 5821 CGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTG 5880
|||||

Db 5341 CGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTG 5400

Qy 5881 TCCTTCGTGCTGACGGCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAG 5940
|||||

Db 5401 TCCTTCGTGCTGACGGCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAG 5460

Qy 5941 CACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAG 6000
|||||

Db 5461 CACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAG 5520

Qy 6001 CTGGAGATGAAGACGCTCAGCCCGAGCCCCACTCCCCGCTGGGCAGCCCCCTTCTCTGG 6060
|||||

Db 5521 CTGGAGATGAAGACGCTCAGCCCGAGCCCCACTCCCCGCTGGGCAGCCCCCTTCTCTGG 5580

Qy 6061 CCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACT 6120
|||||

Db 5581 CCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACT 5640

Qy 6121 GCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACGATGGTACCCACCCCC 6180
|||||

Db 5641 GCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACGATGGTACCCACCCCC 5700

Qy 6181 GAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGAGC 6240
|||||

Db 5701 GAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGAGC 5760

Qy 6241 CGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGAATGGGAGCACTGCTGAGAGA 6300
|||||

Db 5761 CGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGAATGGGAGCACTGCTGAGAGA 5820

Qy 6301 TCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCGGTT 6360
|||||

Db 5821 TCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCGGTT 5880

Qy 6361 CACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTG 6420
|||||

Db 5881 CACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTG 5940

Qy 6421 CTCCAGCCTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGC 6480
|||||

Db 5941 CTCCAGCCTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGC 6000

Qy 6481 TCCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGAT 6540
|||||

Db 6001 TCCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGAT 6060

Qy 6541 GTGCAGGGCCTGGGTAGCCGGAAGACCTGTTGTGTCAGAGGTGAGTGGGCCCTCTGCCCT 6600
|||||

Art Unit: 1646

Db 6061 GTGCAGGGCCTGGGTAGCCGGGAAGACCTGTTGTCAGAGGTGAGTGGGCCCTCCTGCCCT 6120

Qy 6601 CTGACCCGGTCCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGC 6660
|||||

Db 6121 CTGACCCGGTCCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGC 6180

Qy 6661 ATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAACCC 6720
|||||

Db 6181 ATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAACCC 6240

Qy 6721 AGCTGGGCCAAGGACCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGC 6780
|||||

Db 6241 AGCTGGGCCAAGGACCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGC 6300

Qy 6781 TGGATTTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCACGGGACCTG 6840
|||||

Db 6301 TGGATTTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCACGGGACCTG 6360

Qy 6841 AAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGAT 6900
|||||

Db 6361 AAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGAT 6420

Qy 6901 GAACAGCGGAGACACTCCATTGCTGTCTGAGCTGTCTGGACAGCGGCTCCCAACCCCGCCTA 6960
|||||

Db 6421 GAACAGCGGAGACACTCCATTGCTGTCTGAGCTGTCTGGACAGCGGCTCCCAACCCCGCCTA 6480

Qy 6961 TGTCCAAGCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCTGGGAGCCGGCCTAAG 7020
|||||

Db 6481 TGTCCAAGCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCTGGGAGCCGGCCTAAG 6540

Qy 7021 AAAAACTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCC 7080
|||||

Db 6541 AAAAACTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCC 6600

Qy 7081 CCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCC 7140
|||||

Db 6601 CCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCC 6660

Qy 7141 TCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCTCCCCAAAGAAAGACACGCTG 7200
|||||

Db 6661 TCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCTCCCCAAAGAAAGACACGCTG 6720

Qy 7201 AGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 7242
|||||

Db 6721 AGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 6762

RESULT 5

AAX83488

ID AAX83488 standard; cDNA; 6741 BP.

XX

AC AAX83488;

XX

Art Unit: 1646

DT 07-DEC-1999 (first entry)
XX
DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1d) cDNA.
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Rattus sp.
XX
PN W09929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
DR P-PSDB; AAY14593.
XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 94-103; 138pp; English.
XX
CC This sequence represents the coding region for a rat T-type voltage-gated
CC calcium (Ca) channel alpha-1-G designated rCavT1d. Voltage gated channels
CC are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AAX83481-
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC voltage-gated calcium channel proteins can be used to screen for drugs
CC which affect calcium channels. Methods are also disclosed for treating a
CC disease or disorder associated with a deficiency in a native T-type
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6741 BP; 1355 A; 2041 C; 1908 G; 1437 T; 0 U; 0 Other;

Query Match 88.6%; Score 6678.4; DB 2; Length 6741;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 6728; Conservative 0; Mismatches 11; Indels 23; Gaps 2;

Qy 483 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 542
 |||
 Db 1 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 60

Qy 543 CAGCTCAACGACCTGTCCGGGGCCGGGGGC - -GGCAGGGGCCGGGTCGACGGAAAAGGAC 600
 |||
 Db 61 CAGCTCAACGACCTGTCCGGGGCCGGGGGCCGGCAGGGGCCGGGTCGACGGAAAAGGAC 120

Qy	601	CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT	660
Db	121	CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT	180
Qy	661	TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC	720
Db	181	TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC	240
Qy	721	CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG	780
Db	241	CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG	300
Qy	781	TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGATCTGCAGGCCTTC	840
Db	301	TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGATCTGCAGGCCTTC	360
Qy	841	GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC	900
Db	361	GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC	420
Qy	901	ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTC	960
Db	421	ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTC	480
Qy	961	ATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG	1020
Db	481	ATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG	540
Qy	1021	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCAGCATGCGCATTCTC	1080
Db	541	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCAGCATGCGCATTCTC	600
Qy	1081	GTCACATTACTGCTGGACACCTTGCCATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC	1140
Db	601	GTCACATTACTGCTGGACACCTTGCCATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC	660
Qy	1141	GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG	1200
Db	661	GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG	720
Qy	1201	TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG	1260
Db	721	TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG	780
Qy	1261	ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA	1320
Db	781	ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA	840
Qy	1321	TCCTGCAGGAGTGTGCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG	1380
Db	841	TCCTGCAGGAGTGTGCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG	900
Qy	1381	GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT	1440
Db	901	GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT	960
Qy	1441	ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT	1500
Db	961	ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT	1020

Art Unit: 1646

Qy 1501 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACA CTGGAGGGCTGGGTCGACATCATG 1560
| | | | |
Db 1021 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACA CTGGAGGGCTGGGTCGACATCATG 1080

Qy 1561 TACTTCGTAATGGACGCTCACTCCTTCTACA ACTTCATCTACTTCATTCTTCTCATCATC 1620
| | | | |
Db 1081 TACTTCGTAATGGACGCTCACTCCTTCTACA ACTTCATCTACTTCATTCTTCTCATCATC 1140

Qy 1621 GTGGGCTCCTTCTTTCATGATCAACCTGTG CCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1680
| | | | |
Db 1141 GTGGGCTCCTTCTTTCATGATCAACCTGTG CCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1200

Qy 1681 ACCAAACAGCGGGAGAGTCAGCTGATGCG GGAGCAGCGTGACGATTCTGTCCAATGCT 1740
| | | | |
Db 1201 ACCAAACAGCGGGAGAGTCAGCTGATGCG GGAGCAGCGTGACGATTCTGTCCAATGCT 1260

Qy 1741 AGCACCTTGGCAAGCTTCTCTGAGCCAGG CAGCTGCTATGAGGAGCTACTCAAGTACCTG 1800
| | | | |
Db 1261 AGCACCTTGGCAAGCTTCTCTGAGCCAGG CAGCTGCTATGAGGAGCTACTCAAGTACCTG 1320

Qy 1801 GTGTACATCCTCCGAAAAGCAGCCCGAAG GCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1860
| | | | |
Db 1321 GTGTACATCCTCCGAAAAGCAGCCCGAAG GCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1380

Qy 1861 CGGGCTGGGCTGCTCAGCAGCCAGTGGCC CGTAGTGGGCAGGAGCCCCAGCCAGTGGC 1920
| | | | |
Db 1381 CGGGCTGGGCTGCTCAGCAGCCAGTGGCC CGTAGTGGGCAGGAGCCCCAGCCAGTGGC 1440

Qy 1921 AGCTGCACTCGCTCACACCGTCGTCTGT CTGTCCACCACCTGGTCCACCACCATCACCAC 1980
| | | | |
Db 1441 AGCTGCACTCGCTCACACCGTCGTCTGT CTGTCCACCACCTGGTCCACCACCATCACCAC 1500

Qy 1981 CACCATCACC ACTACCACTGGGTAATGGGACGCTCAGAGTTCC CCGGGCCAGCCAGAG 2040
| | | | |
Db 1501 CACCATCACC ACTACCACTGGGTAATGGGACGCTCAGAGTTCC CCGGGCCAGCCAGAG 1560

Qy 2041 ATCCAGGACAGGGATGCCAATGGGTCTCG CCGGCTCATGCTACCACCACCCTCTACACCC 2100
| | | | |
Db 1561 ATCCAGGACAGGGATGCCAATGGGTCTCG CCGGCTCATGCTACCACCACCCTCTACACCC 1620

Qy 2101 ACTCCCTCTGGGGGCCCTCCGAGGGGTG CGGAGTCTGTACACAGCTTCTACCATGCTGAC 2160
| | | | |
Db 1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTG CGGAGTCTGTACACAGCTTCTACCATGCTGAC 1680

Qy 2161 TGCCACTTGGAGCCAGTCCGTTGCCAGGCAC CCCCCTCCAGATGCCCATCGGAGGCATCT 2220
| | | | |
Db 1681 TGCCACTTGGAGCCAGTCCGTTGCCAGGCAC CCCCCTCCAGATGCCCATCGGAGGCATCT 1740

Qy 2221 GG TAGGACTGTGGGTAGTGGGAAGGTGTAC CCCCCTGTGCATACCAGCCCTCCACCAGAG 2280
| | | | |
Db 1741 GG TAGGACTGTGGGTAGTGGGAAGGTGTAC CCCCCTGTGCATACCAGCCCTCCACCAGAG 1800

Qy 2281 ATACTGAAGGATAAAGCACTAGTGGAGGTG GCCCCCAGCCCTGGGCCCCCACCCTCACC 2340
| | | | |
Db 1801 ATACTGAAGGATAAAGCACTAGTGGAGGTG GCCCCCAGCCCTGGGCCCCCACCCTCACC 1860

Qy 2341 AGCTTCAACATCCCACCTGGGCCCTTCAG CTCCATGCACAAGCTCCTGGAGACACAGAGT 2400
| | | | |
Db 1861 AGCTTCAACATCCCACCTGGGCCCTTCAG CTCCATGCACAAGCTCCTGGAGACACAGAGT 1920

Qy	2401	ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGGA	2460
Db	1921	ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGGA	1980
Qy	2461	GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCCGACAGGAGCAGGAGAGCCAGAGTCC	2520
Db	1981	GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCCGACAGGAGCAGGAGAGCCAGAGTCC	2040
Qy	2521	GCTGACCATGTGCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT	2580
Db	2041	GCTGACCATGTGCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT	2100
Qy	2581	CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCAGAT	2640
Db	2101	CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCAGAT	2160
Qy	2641	GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC	2700
Db	2161	GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC	2220
Qy	2701	GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC	2760
Db	2221	GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC	2280
Qy	2761	ATGGGCATCGAGTACCACGAGCAGCCCAGGAGCTACCAACGCCCTGGAAATCAGCAAC	2820
Db	2281	ATGGGCATCGAGTACCACGAGCAGCCCAGGAGCTACCAACGCCCTGGAAATCAGCAAC	2340
Qy	2821	ATCGTCTTCACCAGCCTCTTCGCCTTGAGATGCTGCTGAAACTGCTTGCTACGGTCCC	2880
Db	2341	ATCGTCTTCACCAGCCTCTTCGCCTTGAGATGCTGCTGAAACTGCTTGCTACGGTCCC	2400
Qy	2881	TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCAATTGTGGTCATCAGTGTG	2940
Db	2401	TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCAATTGTGGTCATCAGTGTG	2460
Qy	2941	TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTGCGTGCTGCGGACCTTCCGCCTGATG	3000
Db	2461	TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTGCGTGCTGCGGACCTTCCGCCTGATG	2520
Qy	3001	CGGGTGCTGAAGCTGGTGCCTTCTGCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG	3060
Db	2521	CGGGTGCTGAAGCTGGTGCCTTCTGCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG	2580
Qy	3061	AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTTCATCTTCATCTTC	3120
Db	2581	AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTTCATCTTCATCTTC	2640
Qy	3121	AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG	3180
Db	2641	AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG	2700
Qy	3181	TTGCCAGACCGGAAGAAATTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTAGATT	3240
Db	2701	TTGCCAGACCGGAAGAAATTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTAGATT	2760
Qy	3241	CTGACTCAGGAAGACTGGAATAAAGTCTCTACAACGGCATGGCCTCCACATCGTCTTGG	3300
Db	2761	CTGACTCAGGAAGACTGGAATAAAGTCTCTACAACGGCATGGCCTCCACATCGTCTTGG	2820

Art Unit: 1646

Qy 3301 GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 3360
|||
Db 2821 GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 2880
|||
Qy 3361 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 3420
|||
Db 2881 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 2940
|||
Qy 3421 CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3480
|||
Db 2941 CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3000
|||
Qy 3481 GTGGCTTTGGGAGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3540
|||
Db 3001 GTGGCTTTGGGAGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3060
|||
Qy 3541 ACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3600
|||
Db 3061 ACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3120
|||
Qy 3601 GGCTCTGGCTCTCGACGTACCAAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3660
|||
Db 3121 GGCTCTGGCTCTCGACGTACCAAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3180
|||
Qy 3661 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3720
|||
Db 3181 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3240
|||
Qy 3721 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCAGCCTAAAGCGG 3780
|||
Db 3241 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCAGCCTAAAGCGG 3300
|||
Qy 3781 AGGAGCCCGAGCGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3840
|||
Db 3301 AGGAGCCCGAGCGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3360
|||
Qy 3841 GAGGAGGAAAGTTTCAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3900
|||
Db 3361 GAGGAGGAAAGTTTCAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3420
|||
Qy 3901 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3960
|||
Db 3421 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3480
|||
Qy 3961 GGGCTGCACCGCACAGCCAGCGGCCGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 4020
|||
Db 3481 GGGCTGCACCGCACAGCCAGCGGCCGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 3540
|||
Qy 4021 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCCAACTGGATGGG 4080
|||
Db 3541 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCCAACTGGATGGG 3600
|||
Qy 4081 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCAGA 4140
|||
Db 3601 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCAGA 3660
|||
Qy 4141 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCTGGTTCGGCCTATATCTTTCTCCT 4200
|||
Db 3661 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCTGGTTCGGCCTATATCTTTCTCCT 3720
|||

Qy	4201	CAGTCAAGGTTTCGTCTCCTGTGTACCCGGATCATCACCCACAAGATGTTTGACCATGTG	4260
Db	3721	CAGTCAAGGTTTCGTCTCCTGTGTACCCGGATCATCACCCACAAGATGTTTGACCATGTG	3780
Qy	4261	GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC	4320
Db	3781	GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC	3840
Qy	4321	CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCTCAACTACATCTTCACGGCAGTCTTT	4380
Db	3841	CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCTCAACTACATCTTCACGGCAGTCTTT	3900
Qy	4381	CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC	4440
Db	3901	CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC	3960
Qy	4441	CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC	4500
Db	3961	CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC	4020
Qy	4501	CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG	4560
Db	4021	CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG	4080
Qy	4561	CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCAGGGACTGAAGCTGGTG	4620
Db	4081	CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCAGGGACTGAAGCTGGTG	4140
Qy	4621	GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTGCTGTGCC	4680
Db	4141	GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTGCTGTGCC	4200
Qy	4681	TTCTTCATCATTTTTTGGAAATCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT	4740
Db	4201	TTCTTCATCATTTTTTGGAAATCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT	4260
Qy	4741	CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA	4800
Db	4261	CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA	4320
Qy	4801	TGGGTCCGGCACAAGTACAACCTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG	4860
Db	4321	TGGGTCCGGCACAAGTACAACCTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG	4380
Qy	4861	CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG	4920
Db	4381	CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG	4440
Qy	4921	GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC	4980
Db	4441	GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC	4500
Qy	4981	CTCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGGCGTGGTGGTGGAGAAGTCCAT	5040
Db	4501	CTCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGGCGTGGTGGTGGAGAAGTCCAT	4560
Qy	5041	AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG	5100
Db	4561	AAGTGCAGACAGCACCAGGAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG	4620

Qy	5101	AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGAAGCCCAAGTGCACAGCCC	5160
Db	4621	AGGCTGGAGAAAAAGAGAAGGA-----AAGCCCAGTGCAAGCCC	4659
Qy	5161	TACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTAC	5220
Db	4660	TACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTAC	4719
Qy	5221	CTGGACCTCTTCATCACTGGTGTGCATCGGGCTGAACGTGGTCACTATGGCCATGGAACAT	5280
Db	4720	CTGGACCTCTTCATCACTGGTGTGCATCGGGCTGAACGTGGTCACTATGGCCATGGAACAT	4779
Qy	5281	TACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTC	5340
Db	4780	TACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTC	4839
Qy	5341	ATCTTTGTCTTTGAGTCAGTTTTCAAACCTGTGGCCCTTTGCGTTCCGCCGTTTCTTCCAG	5400
Db	4840	ATCTTTGTCTTTGAGTCAGTTTTCAAACCTGTGGCCCTTTGCGTTCCGCCGTTTCTTCCAG	4899
Qy	5401	GACAGGTGGAACCACTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTG	5460
Db	4900	GACAGGTGGAACCACTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTG	4959
Qy	5461	GAGGAGATTGAGGTCAATCTGTGCGTGCCCATCAACCCACCATCATCCGTATCATGAGG	5520
Db	4960	GAGGAGATTGAGGTCAATCTGTGCGTGCCCATCAACCCACCATCATCCGTATCATGAGG	5019
Qy	5521	GTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTG	5580
Db	5020	GTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTG	5079
Qy	5581	CTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTA	5640
Db	5080	CTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTA	5139
Qy	5641	TTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAG	5700
Db	5140	TTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAG	5199
Qy	5701	ACACACCTTGTGAGGGCTTGGGTGCGCATGCCACCTTTAGGAACCTTGGTATGGCCTTT	5760
Db	5200	ACACACCTTGTGAGGGCTTGGGTGCGCATGCCACCTTTAGGAACCTTGGTATGGCCTTT	5259
Qy	5761	CTGACCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACCCTTCC	5820
Db	5260	CTGACCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACCCTC	5319
Qy	5821	CGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTG	5880
Db	5320	CGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTG	5379
Qy	5881	TCCTTCGTGCTGACGGCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAG	5940
Db	5380	TCCTTCGTGCTGACGGCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAG	5439
Qy	5941	CACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAG	6000
Db	5440	CACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAG	5499

Art Unit: 1646

Qy	6001	CTGGAGATGAAGACGCTCAGCCCCGAGCCCCCACTCCCCGCTGGGCAGCCCTTCTCTCTGG	6060
Db	5500	CTGGAGATGAAGACGCTCAGCCCCGAGCCCCCACTCCCCGCTGGGCAGCCCTTCTCTCTGG	5559
Qy	6061	CCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACT	6120
Db	5560	CCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACT	5619
Qy	6121	GCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACGATGGTACCCACCCC	6180
Db	5620	GCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACGATGGTACCCACCCC	5679
Qy	6181	GAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGAGC	6240
Db	5680	GAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGAGC	5739
Qy	6241	CGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGA	6300
Db	5740	CGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGA	5799
Qy	6301	TCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTT	6360
Db	5800	TCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTT	5859
Qy	6361	CACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTG	6420
Db	5860	CACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTG	5919
Qy	6421	CTCCAGCCTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGC	6480
Db	5920	CTCCAGCCTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGC	5979
Qy	6481	TCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGAT	6540
Db	5980	TCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGAT	6039
Qy	6541	GTGCAGGGCCTGGGTAGCCGGAAGACCTGTTGTGTCAGAGGTGAGTGGGCCCTCCTGCCCT	6600
Db	6040	GTGCAGGGCCTGGGTAGCCGGAAGACCTGTTGTGTCAGAGGTGAGTGGGCCCTCCTGCCCT	6099
Qy	6601	CTGACCCGGTCTCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGGTTCCGGC	6660
Db	6100	CTGACCCGGTCTCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGGTTCCGGC	6159
Qy	6661	ATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCCTTGCCCAGGCCTGGAACCC	6720
Db	6160	ATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCCTTGCCCAGGCCTGGAACCC	6219
Qy	6721	AGCTGGGCCAAGGACCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGC	6780
Db	6220	AGCTGGGCCAAGGACCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGC	6279
Qy	6781	TGGATTTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCCACGGGACCTG	6840
Db	6280	TGGATTTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCCACGGGACCTG	6339
Qy	6841	AAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGAT	6900
Db	6340	AAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGAT	6399

Qy	6901	GAACAGCGGAGACACTCCATTGCTGTCACTGTCTGGACAGCGGCTCCCCAACCCCGCCTA	6960
Db	6400	GAACAGCGGAGACACTCCATTGCTGTCACTGTCTGGACAGCGGCTCCCCAACCCCGCCTA	6459
Qy	6961	TGTCCAAGCCCCTCAAGCCTCGGGGGCCAACTCTTGGGGGTCCTGGGAGCCGGCCTAAG	7020
Db	6460	TGTCCAAGCCCCTCAAGCCTCGGGGGCCAACTCTTGGGGGTCCTGGGAGCCGGCCTAAG	6519
Qy	7021	AAAAAACTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCC	7080
Db	6520	AAAAAACTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCC	6579
Qy	7081	CCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCC	7140
Db	6580	CCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCC	6639
Qy	7141	TCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCTCCCCAAAGAAAGACACGCTG	7200
Db	6640	TCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCTCCCCAAAGAAAGACACGCTG	6699
Qy	7201	AGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC	7242
Db	6700	AGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC	6741

RESULT 6

AAX83486

ID AAX83486 standard; cDNA; 6795 BP.

XX

AC AAX83486;

XX

DT 07-DEC-1999 (first entry)

XX

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1b) cDNA.

XX

KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

XX

OS Rattus sp.

XX

PN WO9929847-A1.

XX

PD 17-JUN-1999.

XX

PF 30-OCT-1998; 98WO-US023161.

XX

PR 05-DEC-1997; 97US-00985809.

XX

PA (LOYO) UNIV LOYOLA CHICAGO.

XX

PI Perez-Reyes E, . Cribbs LL;

XX

DR WPI; 1999-394972/33.

DR P-PSDB; AAY14591.

Art Unit: 1646

XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 76-85; 138pp; English.
XX
CC This sequence represents the coding region for a rat T-type voltage-gated
CC calcium (Ca) channel alpha-1-G designated rCavT1b. Voltage gated channels
CC are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AAX83481-
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC voltage-gated calcium channel proteins can be used to screen for drugs
CC which affect calcium channels. Methods are also disclosed for treating a
CC disease or disorder associated with a deficiency in a native T-type
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6795 BP; 1366 A; 2055 C; 1923 G; 1451 T; 0 U; 0 Other;

Query Match 88.4%; Score 6665; DB 2; Length 6795;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 6735; Conservative 0; Mismatches 25; Indels 35; Gaps 2;

Qy	483	ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG	542
Db	1	ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG	60
Qy	543	CAGCTCAACGACCTGTCCGGGGCCGGGGGC -- GGCAGGGGCCGGGTCGACGAAAAGGAC	600
Db	61	CAGCTCAACGACCTGTCCGGGGCCGGGGGCCGCGAGGGGCCGGGTCGACGAAAAGGAC	120
Qy	601	CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT	660
Db	121	CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT	180
Qy	661	TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC	720
Db	181	TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC	240
Qy	721	CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG	780
Db	241	CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG	300
Qy	781	TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC	840
Db	301	TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC	360
Qy	841	GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC	900
Db	361	GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC	420
Qy	901	ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGAACCGGCTTGACTTTTTTCATTGTC	960
Db	421	ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGAACCGGCTTGACTTTTTTCATTGTC	480

Qy	961	ATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG	1020
Db	481	ATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG	540
Qy	1021	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCAGCATGCGCATTCTC	1080
Db	541	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCAGCATGCGCATTCTC	600
Qy	1081	GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC	1140
Db	601	GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC	660
Qy	1141	GTCTTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG	1200
Db	661	GTCTTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG	720
Qy	1201	TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG	1260
Db	721	TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG	780
Qy	1261	ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA	1320
Db	781	ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA	840
Qy	1321	TCCTGCAGGAGTGTGCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG	1380
Db	841	TCCTGCAGGAGTGTGCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG	900
Qy	1381	GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT	1440
Db	901	GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT	960
Qy	1441	ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT	1500
Db	961	ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT	1020
Qy	1501	GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG	1560
Db	1021	GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG	1080
Qy	1561	TACTTCGTAATGGACGCTCACTCCTTCTACAACCTTCATCTACTTCATTCTTCTCATCATC	1620
Db	1081	TACTTCGTAATGGACGCTCACTCCTTCTACAACCTTCATCTACTTCATTCTTCTCATCATC	1140
Qy	1621	GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG	1680
Db	1141	GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG	1200
Qy	1681	ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCTGTCCAATGCT	1740
Db	1201	ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCTGTCCAATGCT	1260
Qy	1741	AGCACCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG	1800
Db	1261	AGCACCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG	1320
Qy	1801	GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG	1860
Db	1321	GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG	1380

Qy	1861	CGGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCAGTGGC	1920
Db	1381	CGGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCAGTGGC	1440
Qy	1921	AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC	1980
Db	1441	AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC	1500
Qy	1981	CACCATCACCCTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG	2040
Db	1501	CACCATCACCCTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG	1560
Qy	2041	ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCTCTACACCC	2100
Db	1561	ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCTCTACACCC	1620
Qy	2101	ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC	2160
Db	1621	ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC	1680
Qy	2161	TGCCACTTGAGCCAGTCCGTTGCCAGGCACCCCCTCCAGATGCCCATCGGAGGCATCT	2220
Db	1681	TGCCACTTGAGCCAGTCCGTTGCCAGGCACCCCCTCCAGATGCCCATCGGAGGCATCT	1740
Qy	2221	GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG	2280
Db	1741	GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG	1800
Qy	2281	ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACC	2340
Db	1801	ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACC	1860
Qy	2341	AGCTTCAACATCCCACCTGGGCCCTTCAGTCCATGCACAAGCTCCTGGAGACACAGAGT	2400
Db	1861	AGCTTCAACATCCCACCTGGGCCCTTCAGTCCATGCACAAGCTCCTGGAGACACAGAGT	1920
Qy	2401	ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGGA	2460
Db	1921	ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGGA	1980
Qy	2461	GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC	2520
Db	1981	GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC	2040
Qy	2521	GCTGACCATGTGCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT	2580
Db	2041	GCTGACCATGTGCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT	2100
Qy	2581	CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCCAGAT	2640
Db	2101	CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCCAGAT	2160
Qy	2641	GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC	2700
Db	2161	GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC	2220
Qy	2701	GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC	2760
Db	2221	GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC	2280

Qy	2761	ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC	2820
Db	2281	ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC	2340
Qy	2821	ATCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGCTGAAACTGCTTGCTACGGTCCC	2880
Db	2341	ATCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGCTGAAACTGCTTGCTACGGTCCC	2400
Qy	2881	TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCTATTGTGGTCATCAGTGTG	2940
Db	2401	TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCTATTGTGGTCATCAGTGTG	2460
Qy	2941	TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTGCGTGCTGCGGACCTTCCGCCTGATG	3000
Db	2461	TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTGCGTGCTGCGGACCTTCCGCCTGATG	2520
Qy	3001	CGGGTGCTGAAGCTGGTGCCTTCTGCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG	3060
Db	2521	CGGGTGCTGAAGCTGGTGCCTTCTGCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG	2580
Qy	3061	AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTTCATCTTCATCTTC	3120
Db	2581	AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTTCATCTTCATCTTC	2640
Qy	3121	AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG	3180
Db	2641	AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG	2700
Qy	3181	TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTTCAGATT	3240
Db	2701	TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTTCAGATT	2760
Qy	3241	CTGACTCAGGAAGACTGGAATAAAGTCTCTACAACGGCATGGCCTCCACATCGTCTTGG	3300
Db	2761	CTGACTCAGGAAGACTGGAATAAAGTCTCTACAACGGCATGGCCTCCACATCGTCTTGG	2820
Qy	3301	GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG	3360
Db	2821	GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG	2880
Qy	3361	GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG	3420
Db	2881	GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG	2940
Qy	3421	CCTGATTCTTTTCGCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG	3480
Db	2941	CCTGATTCTTTTCGCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG	3000
Qy	3481	GTGGCTTTGGGAGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT	3540
Db	3001	GTGGCTTTGGGAGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT	3060
Qy	3541	ACGGCTGCGACACCAATGTACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG	3600
Db	3061	ACGGCTGCGACACCAATGTACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG	3120
Qy	3601	GGCTCTGGCTCTCGACGTACCAAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT	3660
Db	3121	GGCTCTGGCTCTCGACGTACCAAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT	3180

Art Unit: 1646

Qy 3661 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3720
| | | | |
Db 3181 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3240
| | | | |

Qy 3721 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCAGCCTAAAGCGG 3780
| | | | |
Db 3241 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCAGCCTAAAGCGG 3300
| | | | |

Qy 3781 AGGAGCCCGAGCGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3840
| | | | |
Db 3301 AGGAGCCCGAGCGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3360
| | | | |

Qy 3841 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCAGCAGGCAGTGACCATCGCCACAGG 3900
| | | | |
Db 3361 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCAGCAGGCAGTGACCATCGCCACAGG 3420
| | | | |

Qy 3901 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3960
| | | | |
Db 3421 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3480
| | | | |

Qy 3961 GGGCTGCACCGCACAGCCAGCGGCCGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 4020
| | | | |
Db 3481 GGGCTGCACCGCACAGCCAGCGGCCGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 3540
| | | | |

Qy 4021 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCCAACTGGATGGG 4080
| | | | |
Db 3541 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCCAACTGGATGGG 3600
| | | | |

Qy 4081 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTGAGA 4140
| | | | |
Db 3601 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTGAGA 3660
| | | | |

Qy 4141 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCTGGTTCGGCCTATATCTTTCCTCCT 4200
| | | | |
Db 3661 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCTGGTTCGGCCTATATCTTTCCTCCT 3720
| | | | |

Qy 4201 CAGTCAAGGTTTTCGTCTCCTGTGTACCCGATCATCACCACAAAGATGTTTGACCATGTG 4260
| | | | |
Db 3721 CAGTCAAGGTTTTCGTCTCCTGTGTACCCGATCATCACCACAAAGATGTTTGACCATGTG 3780
| | | | |

Qy 4261 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 4320
| | | | |
Db 3781 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 3840
| | | | |

Qy 4321 CCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACCTACATCTTCACGGCAGTCTTT 4380
| | | | |
Db 3841 CCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACCTACATCTTCACGGCAGTCTTT 3900
| | | | |

Qy 4381 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 4440
| | | | |
Db 3901 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 3960
| | | | |

Qy 4441 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC 4500
| | | | |
Db 3961 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC 4020
| | | | |

Qy 4501 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4560
| | | | |
Db 4021 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4080
| | | | |

Qy	4561	CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCAGGGACTGAAGCTGGTG	4620
Db	4081	CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCAGGGACTGAAGCTGGTG	4140
Qy	4621	GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC	4680
Db	4141	GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC	4200
Qy	4681	TTCTTCATCATTTTTTGGAAATCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT	4740
Db	4201	TTCTTCATCATTTTTTGGAAATCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT	4260
Qy	4741	CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA	4800
Db	4261	CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA	4320
Qy	4801	TGGGTCCGGCACAAGTACAACCTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG	4860
Db	4321	TGGGTCCGGCACAAGTACAACCTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG	4380
Qy	4861	CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG	4920
Db	4381	CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG	4440
Qy	4921	GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC	4980
Db	4441	GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC	4500
Qy	4981	CTCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT	5040
Db	4501	CTCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT	4560
Qy	5041	AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG	5100
Db	4561	AAGTGCAGACAGCACCAGGAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG	4620
Qy	5101	AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCA-----	5135
Db	4621	AGGCTGGAGAAAAAGAGAAGGAATCTAATGTTGGACGATGTAATTGCTTCCGGCAGCTCA	4680
Qy	5136	-----GATGGCCGAAGCCAGTGCAAGCCCTACTACTCTGACTACTCGAGATTCCGG	5187
Db	4681	GCCAGCGCTGCGTCAGAAGCCAGTGCAAGCCCTACTACTCTGACTACTCGAGATTCCGG	4740
Qy	5188	CTCCTTGTCACACCTGTGTACCAGCCACTACCTGGACCTCTTCATCACTGGTGTATC	5247
Db	4741	CTCCTTGTCACACCTGTGTACCAGCCACTACCTGGACCTCTTCATCACTGGTGTATC	4800
Qy	5248	GGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAGCAGCCCCAGATCCTGGACGAG	5307
Db	4801	GGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAGCAGCCCCAGATCCTGGACGAG	4860
Qy	5308	GCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTTGTCTTTGAGTCAGTTTTCAA	5367
Db	4861	GCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTTGTCTTTGAGTCAGTTTTCAA	4920
Qy	5368	CTTGTGGCCTTTGCGTTCCGCCGTTTCTTCCAGGACAGGTGGAACCAGCTGGACCTGGCT	5427
Db	4921	CTTGTGGCCTTTGCGTTCCGCCGTTTCTTCCAGGACAGGTGGAACCAGCTGGACCTGGCT	4980

Qy	5428	ATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATCTGTGCGTG	5487
Db	4981	ATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATCTGTGCGTG	5040
Qy	5488	CCCATCAACCCCAACCATCATCCGTATCATGAGGGTGCTCCGCATTGCTCGAGTTCTGAAG	5547
Db	5041	CCCATCAACCCCAACCATCATCCGTATCATGAGGGTGCTCCGCATTGCTCGAGTTCTGAAG	5100
Qy	5548	CTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGCACACGGTGATGCAGGCCCTGCC	5607
Db	5101	CTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGCACACGGTGATGCAGGCCCTGCC	5160
Qy	5608	CAGGTGGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTCATCTTTGCAGCTCTGGGC	5667
Db	5161	CAGGTGGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTCATCTTTGCAGCTCTGGGC	5220
Qy	5668	GTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGTGAGGGCTTGGGTCGG	5727
Db	5221	GTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGTGAGGGCTTGGGTCGG	5280
Qy	5728	CATGCCACCTTTAGGAACCTTGGTATGGCCTTCTGACCCTCTTCCGAGTCTCCACTGGT	5787
Db	5281	CATGCCACCTTTAGGAACCTTGGTATGGCCTTCTGACCCTCTTCCGAGTCTCCACTGGT	5340
Qy	5788	GACAACTGGAATGGTATTATGAAGGACCCCTCCCGGGACTGTGACCAGGAGTCCACCTGC	5847
Db	5341	GACAACTGGAATGGTATTATGAAGGACCCCTCCCGGGACTGTGACCAGGAGTCCACCTGC	5400
Qy	5848	TACAACACTGTCATCTCCCTATCTACTTTGTGTCTTCGTGCTGACGGCCAGTTTGTG	5907
Db	5401	TACAACACTGTCATCTCCCTATCTACTTTGTGTCTTCGTGCTGACGGCCAGTTTGTG	5460
Qy	5908	CTGGTCAACGTGGTCATAGCTGTGCTGATGAAGCACCTGGAAGAAAGCAACAAAGAGGCC	5967
Db	5461	CTGGTCAACGTGGTCATAGCTGTGCTGATGAAGCACCTGGAAGAAAGCAACAAAGAGGCC	5520
Qy	5968	AAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCCCGCAG	6027
Db	5521	AAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCCCGCAG	5580
Qy	6028	CCCCACTCCCCGCTGGGCAGCCCCCTTCCTCTGGCCCCGGGTGGAGGGTGTCAACAGTACT	6087
Db	5581	CCCCACTCCCCGCTGGGCAGCCCCCTTCCTCTGGCCCCGGGTGGAGGGTGTCAACAGTACT	5640
Qy	6088	GACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCCTCGGGCTTC	6147
Db	5641	GACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCCTCGGGCTTC	5700
Qy	6148	TCCCTTGAGCACCCACGATGGTAACCCACCCGAGGAGGTGCCAGTCCCCCTAGGACCA	6207
Db	5701	TCCCTTGAGCACCCACGATGGTAACCCACCCGAGGAGGTGCCAGTCCCCCTAGGACCA	5760
Qy	6208	GACCTGCTGACTGTGAGGAAGTCTGGTGTGAGCCGGACGCACTCTCTGCCAATGACAGC	6267
Db	5761	GACCTGCTGACTGTGAGGAAGTCTGGTGTGAGCCGGACGCACTCTCTGCCAATGACAGC	5820
Qy	6268	TACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGGGCTGGGGGCTC	6327
Db	5821	TACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGGGCTGGGGGCTC	5880

Qy	6328	CCCAAAGCCAGTCAGGCTCCATCTTGTCCGTTCACTCCCAACCAGCAGACACCAGCTGC	6387
Db	5881	CCCAAAGCCAGTCAGGCTCCATCTTGTCCGTTCACTCCCAACCAGCAGACACCAGCTGC	5940
Qy	6388	ATCCTACAGCTTCCCAAAGATGTGCACTATCTGCTCCAGCCTCATGGGGCTCCACCTGG	6447
Db	5941	ATCCTACAGCTTCCCAAAGATGTGCACTATCTGCTCCAGCCTCATGGGGCTCCACCTGG	6000
Qy	6448	GGCGCCATCCCTAAACTACCCCCACCTGGCCGCTCCCCTCTGGCTCAGAGGCCTCTCAGG	6507
Db	6001	GGCGCCATCCCTAAACTACCCCCACCTGGCCGCTCCCCTCTGGCTCAGAGGCCTCTCAGG	6060
Qy	6508	CGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGCAGGGCCTGGGTAGCCGGGAAGAC	6567
Db	6061	CGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGCAGGGCCTGGGTAGCCGGGAAGAC	6120
Qy	6568	CTGTTGTCTAGAGGTGAGTGGGCCCTCCTGCCCTCTGACCCGGTCCTCATCCTTCTGGGGC	6627
Db	6121	CTGTTGTCTAGAGGTGAGTGGGCCCTCCTGCCCTCTGACCCGGTCCTCATCCTTCTGGGGC	6180
Qy	6628	GGGTCGAGCATCCAGGTGCAGCAGCGTTCGGGCATCCAGAGCAAAGTCTCCAAGCACATC	6687
Db	6181	GGGTCGAGCATCCAGGTGCAGCAGCGTTCGGGCATCCAGAGCAAAGTCTCCAAGCACATC	6240
Qy	6688	CGCCTGCCAGCCCCCTTGCCCAGGCCTGGAACCCAGCTGGGCCAAGGACCCTCCAGAGACC	6747
Db	6241	CGCCTGCCAGCCCCCTTGCCCAGGCCTGGAACCCAGCTGGGCCAAGGACCCTCCAGAGACC	6300
Qy	6748	AGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCCTTCCCAGC	6807
Db	6301	AGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCCTTCCCAGC	6360
Qy	6808	AGCCAGGAAGAACCCTGTTCACGGGACCTGAAGAAGTGCTACAGTGTAGAGACCCAG	6867
Db	6361	AGCCAGGAAGAACCCTGTTCACGGGACCTGAAGAAGTGCTACAGTGTAGAGACCCAG	6420
Qy	6868	AGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGATGAACAGCGGAGACACTCCATTGCTGTC	6927
Db	6421	AGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGATGAACAGCGGAGACACTCCATTGCTGTC	6480
Qy	6928	AGCTGTCTGGACAGCGGCTCCCAACCCCGCTATGTCCAAGCCCCTCAAGCCTCGGGGGC	6987
Db	6481	AGCTGTCTGGACAGCGGCTCCCAACCCCGCTATGTCCAAGCCCCTCAAGCCTCGGGGGC	6540
Qy	6988	CAACCTCTTGGGGGTCCTGGGAGCCGGCCTAAGAAAAAACTCAGCCCACCCAGTATCTCT	7047
Db	6541	CAACCTCTTGGGGGTCCTGGGAGCCGGCCTAAGAAAAAACTCAGCCCACCCAGTATCTCT	6600
Qy	7048	ATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCAGTCCTGGTGTCTGCCTCAGG	7107
Db	6601	ATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCAGTCCTGGTGTCTGCCTCAGG	6660
Qy	7108	AGGAGGGCGCCGGCCAGTGACTCTAAGGATCCCTCGGTCTCCAGCCCCCTTGACAGCACG	7167
Db	6661	AGGAGGGCGCCGGCCAGTGACTCTAAGGATCCCTCGGTCTCCAGCCCCCTTGACAGCACG	6720
Qy	7168	GCTGCCTCACCTCCCCAAAGAAAGACACGCTGAGTCTCTCTGGTTTGTCTTCTGACCCA	7227
Db	6721	GCTGCCTCACCTCCCCAAAGAAAGACACGCTGAGTCTCTCTGGTTTGTCTTCTGACCCA	6780

Art Unit: 1646

Qy 7228 ACAGACATGGACCCC 7242
 |||||
Db 6781 ACAGACATGGACCCC 6795

RESULT 7

AAX83487

ID AAX83487 standard; cDNA; 6816 BP.

XX

AC AAX83487;

XX

DT 07-DEC-1999 (first entry)

XX

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1c) cDNA.

XX

KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

XX

OS Rattus sp.

XX

PN WO9929847-A1.

XX

PD 17-JUN-1999.

XX

PF 30-OCT-1998; 98WO-US023161.

XX

PR 05-DEC-1997; 97US-00985809.

XX

PA (LOYO) UNIV LOYOLA CHICAGO.

XX

PI Perez-Reyes E, Cribbs LL;

XX

DR WPI; 1999-394972/33.

DR P-PSDB; AAY14592.

XX

PT New T-type voltage-gated calcium channels.

XX

PS Disclosure; Page 85-94; 138pp; English.

XX

CC This sequence represents the coding region for a rat T-type voltage-gated
CC calcium (Ca) channel alpha-1-G designated rCavT1c. Voltage gated channels
CC are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AAX83481-
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC voltage-gated calcium channel proteins can be used to screen for drugs
CC which affect calcium channels. Methods are also disclosed for treating a
CC disease or disorder associated with a deficiency in a native T-type
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX

SQ Sequence 6816 BP; 1373 A; 2058 C; 1932 G; 1453 T; 0 U; 0 Other;

Art Unit: 1646

Query Match 88.4%; Score 6661.6; DB 2; Length 6816;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 6746; Conservative 0; Mismatches 14; Indels 56; Gaps 2;

```
Qy      483 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 542
          |||
Db      1  ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 60

Qy      543 CAGCTCAACGACCTGTCCGGGGCCGGGGGC--GGCAGGGGCCGGGTCGACGAAAAGGAC 600
          |||
Db      61 CAGCTCAACGACCTGTCCGGGGCCGGGGGCCGCGAGGGGCCGGGTCGACGAAAAGGAC 120

Qy      601 CCGGGCAGCGCGGACTCCGAGGCGGAGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 660
          |||
Db      121 CCGGGCAGCGCGGACTCCGAGGCGGAGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 180

Qy      661 TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 720
          |||
Db      181 TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 240

Qy      721 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 780
          |||
Db      241 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 300

Qy      781 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCCTTC 840
          |||
Db      301 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCCTTC 360

Qy      841 GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 900
          |||
Db      361 GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 420

Qy      901 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGAACCGGCTTGACTTTTTTCATTGTC 960
          |||
Db      421 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGAACCGGCTTGACTTTTTTCATTGTC 480

Qy      961 ATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 1020
          |||
Db      481 ATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 540

Qy      1021 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCAGCATGCGCATTCTC 1080
          |||
Db      541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCAGCATGCGCATTCTC 600

Qy      1081 GTCACATTACTGCTGGACACCTTGCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 1140
          |||
Db      601 GTCACATTACTGCTGGACACCTTGCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 660

Qy      1141 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 1200
          |||
Db      661 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 720

Qy      1201 TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 1260
          |||
Db      721 TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 780

Qy      1261 ACAGAGAATGAGGACGAGAGCCCCCTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGA 1320
          |||
Db      781 ACAGAGAATGAGGACGAGAGCCCCCTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGA 840
```

Art Unit: 1646

Qy 1321 TCCTGCAGGAGTGTGCCCACACTGCGTGGGGAAGGCGGTGGTGGCCACCCCTGCAGTCTG 1380
| | | | |
Db 841 TCCTGCAGGAGTGTGCCCACACTGCGTGGGGAAGGCGGTGGTGGCCACCCCTGCAGTCTG 900
| | | | |

Qy 1381 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 1440
| | | | |
Db 901 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 960
| | | | |

Qy 1441 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1500
| | | | |
Db 961 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1020
| | | | |

Qy 1501 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1560
| | | | |
Db 1021 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1080
| | | | |

Qy 1561 TACTTCGTAATGGACGCTCACTCCTTCTACAACCTTCATCTACTTCATTCTTCTCATCATC 1620
| | | | |
Db 1081 TACTTCGTAATGGACGCTCACTCCTTCTACAACCTTCATCTACTTCATTCTTCTCATCATC 1140
| | | | |

Qy 1621 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1680
| | | | |
Db 1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1200
| | | | |

Qy 1681 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGACGATTCTGTCCAATGCT 1740
| | | | |
Db 1201 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGACGATTCTGTCCAATGCT 1260
| | | | |

Qy 1741 AGCACCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1800
| | | | |
Db 1261 AGTACCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1320
| | | | |

Qy 1801 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCAGGTCTCTAGGGCTATAGGCGTG 1860
| | | | |
Db 1321 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCAGGTCTCTAGGGCTATAGGCGTG 1380
| | | | |

Qy 1861 CGGGCTGGGCTGCTCAGCAGCCAGTGCGCCGCTAGTGGGCAGGAGCCCCAGCCAGTGCC 1920
| | | | |
Db 1381 CGGGCTGGGCTGCTCAGCAGCCAGTGCGCCGCTAGTGGGCAGGAGCCCCAGCCAGTGCC 1440
| | | | |

Qy 1921 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1980
| | | | |
Db 1441 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1500
| | | | |

Qy 1981 CACCATCACCACCTACCACCTGGGTAATGGGACGCTCAGAGTCCCCGGGCCAGCCAGAG 2040
| | | | |
Db 1501 CACCATCACCACCTACCACCTGGGTAATGGGACGCTCAGAGTCCCCGGGCCAGCCAGAG 1560
| | | | |

Qy 2041 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGTACCACCACCCTCTACACCC 2100
| | | | |
Db 1561 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGTACCACCACCCTCTACACCC 1620
| | | | |

Qy 2101 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 2160
| | | | |
Db 1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 1680
| | | | |

Qy 2161 TGCCACTTGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCT 2220
| | | | |
Db 1681 TGCCACTTGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCT 1740
| | | | |

Art Unit: 1646

Qy	2221	GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG	2280
Db	1741	GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG	1800
Qy	2281	ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCTCACC	2340
Db	1801	ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCACCTCACC	1860
Qy	2341	AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT	2400
Db	1861	AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT	1920
Qy	2401	ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGGA	2460
Db	1921	ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGGA	1980
Qy	2461	GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC	2520
Db	1981	GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC	2040
Qy	2521	GCTGACCATGTGCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT	2580
Db	2041	GCTGACCATGTGCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT	2100
Qy	2581	CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCAGACGGAGCCTGGGCCCAGAT	2640
Db	2101	CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCAGACGGAGCCTGGGCCCAGAT	2160
Qy	2641	GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC	2700
Db	2161	GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC	2220
Qy	2701	GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC	2760
Db	2221	GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC	2280
Qy	2761	ATGGGCATCGAGTACCACGAGCAGCCCAGGAGCTACCAACGCCCTGGAAATCAGCAAC	2820
Db	2281	ATGGGCATCGAGTACCACGAGCAGCCCAGGAGCTACCAACGCCCTGGAAATCAGCAAC	2340
Qy	2821	ATCGTCTTCACCAGCCTCTTCGCCTTGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC	2880
Db	2341	ATCGTCTTCACCAGCCTCTTCGCCTTGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC	2400
Qy	2881	TTTGGCTACATTAAGAAATCCCTACAACATCTTTGATGGTGTGCTTGTGGTTCATCAGTGTG	2940
Db	2401	TTTGGCTACATTAAGAAATCCCTACAACATCTTTGATGGTGTGCTTGTGGTTCATCAGTGTG	2460
Qy	2941	TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGATG	3000
Db	2461	TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGATG	2520
Qy	3001	CGGGTGCTGAAGCTGGTGCCTTCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG	3060
Db	2521	CGGGTGCTGAAGCTGGTGCCTTCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG	2580
Qy	3061	AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTTCATCTTCATCTTC	3120
Db	2581	AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTTCATCTTCATCTTC	2640

Qy	3121	AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTTCGCATCTGAACGGGATGGGGACACG	3180
Db	2641	AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTTCGCATCTGAACGGGATGGGGACACG	2700
Qy	3181	TTGCCAGACCGGAAGAATTTGCACTCCCTGCTCTGGGCCATCGTCACTGTCTTTAGATT	3240
Db	2701	TTGCCAGACCGGAAGAATTTGCACTCCCTGCTCTGGGCCATCGTCACTGTCTTTAGATT	2760
Qy	3241	CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG	3300
Db	2761	CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG	2820
Qy	3301	GCTGCTCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG	3360
Db	2821	GCTGCTCTTTACTTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG	2880
Qy	3361	GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG	3420
Db	2881	GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG	2940
Qy	3421	CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG	3480
Db	2941	CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG	3000
Qy	3481	GTGGCTTTGGGAGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT	3540
Db	3001	GTGGCTTTGGGAGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT	3060
Qy	3541	ACGGCTGCGACACCAATGTACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG	3600
Db	3061	ACGGCTGCGACACCAATGTACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG	3120
Qy	3601	GGCTCTGGCTCTCGACGTACCAAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCACCAT	3660
Db	3121	GGCTCTGGCTCTCGACGTACCAAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCACCAT	3180
Qy	3661	GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCGCACAGTCCCTGGAGTGCAGCAAGC	3720
Db	3181	GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCGCACAGTCCCTGGAGTGCAGCAAGC	3240
Qy	3721	AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGGCCCCAGCCTAAAGCGG	3780
Db	3241	AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGGCCCCAGCCTAAAGCGG	3300
Qy	3781	AGGAGCCCAGCAGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT	3840
Db	3301	AGGAGCCCAGCAGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT	3360
Qy	3841	GAGGAGGAAAGTTTCAGAAGAGGACCGGGCCAGCCAGCAGGCAGTGACCATCGCCACAGG	3900
Db	3361	GAGGAGGAAAGTTTCAGAAGAGGACCGGGCCAGCCAGCAGGCAGTGACCATCGCCACAGG	3420
Qy	3901	GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG	3960
Db	3421	GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG	3480
Qy	3961	GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC	4020
Db	3481	GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC	3540

Qy	4021	AAGTCGGCTTCAGGGCGTTTGGCCCGCACCCCTGAGGACTGATGACCCCCAACTGGATGGG	4080
Db	3541	AAGTCGGCTTCAGGGCGTTTGGCCCGCACCCCTGAGGACTGATGACCCCCAACTGGATGGG	3600
Qy	4081	GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCAGA	4140
Db	3601	GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCAGACAAGCCTGGGTCAGA	3660
Qy	4141	TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCTGGTCGGCCTATATCTTTCCTCCT	4200
Db	3661	TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCTGGTCGGCCTATATCTTTCCTCCT	3720
Qy	4201	CAGTCAAGGTTTCGTCTCCTGTGTACCGGATCATCACCCACAAGATGTTTGACCATGTG	4260
Db	3721	CAGTCAAGGTTTCGTCTCCTGTGTACCGGATCATCACCCACAAGATGTTTGACCATGTG	3780
Qy	4261	GTCTCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC	4320
Db	3781	GTCTCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC	3840
Qy	4321	CCCCACAGCGCTGAGCGCATCTTCTGACCCTCTCCAACACATCTTCACGGCAGTCTTT	4380
Db	3841	CCCCACAGCGCTGAGCGCATCTTCTGACCCTCTCCAACACATCTTCACGGCAGTCTTT	3900
Qy	4381	CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC	4440
Db	3901	CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC	3960
Qy	4441	CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC	4500
Db	3961	CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC	4020
Qy	4501	CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG	4560
Db	4021	CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG	4080
Qy	4561	CTGCTGCGGACCCTGCGTCCAACCTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG	4620
Db	4081	CTGCTGCGGACCCTGCGTCCAACCTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG	4140
Qy	4621	GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC	4680
Db	4141	GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC	4200
Qy	4681	TTCTTCATCATTTTTTGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT	4740
Db	4201	TTCTTCATCATTTTTTGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT	4260
Qy	4741	CAGGGTGAGGACACCAGGAACATCACTAACAATCCGACTGCGCTGAGGCCAGCTACCGA	4800
Db	4261	CAGGGTGAGGACACCAGGAACATCACTAACAATCCGACTGCGCTGAGGCCAGCTACCGA	4320
Qy	4801	TGGGTCCGGCACAAGTACAACCTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG	4860
Db	4321	TGGGTCCGGCACAAGTACAACCTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG	4380
Qy	4861	CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG	4920
Db	4381	CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG	4440

Qy	4921	GATCAGCAGCCCCATCATGAACCACAACCCCTGGATGTCTGCTATACTTCATCTCCTTCCCTC	4980
Db	4441	GATCAGCAGCCCCATCATGAACCACAACCCCTGGATGTCTGCTATACTTCATCTCCTTCCCTC	4500
Qy	4981	CTCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT	5040
Db	4501	CTCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT	4560
Qy	5041	AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGGAGGCGCGTGAGGAGAAGCGACTACGG	5100
Db	4561	AAGTGCAGACAGCACCAGGAGGAGGAGGAGGAGGCGGAGGCGCGTGAGGAGAAGCGACTACGG	4620
Qy	5101	AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCC-----	5142
Db	4621	AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGATCTAATGTTGGACGAT	4680
Qy	5143	-----GAAGCCCAGTGCAAGCCCTACTAC	5166
Db	4681	GTAATTGCTTCCGGCAGCTCAGCCAGCGCTGCGTCAGAAGCCCAGTGCAAGCCCTACTAC	4740
Qy	5167	TCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTACCTGGAC	5226
Db	4741	TCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTACCTGGAC	4800
Qy	5227	CTCTTCATCACTGGTGTTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAG	5286
Db	4801	CTCTTCATCACTGGTGTTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAG	4860
Qy	5287	CAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTT	5346
Db	4861	CAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTT	4920
Qy	5347	GTCTTTGAGTCAGTTTTCAAACCTTGTGGCCTTTGCGTTCCGCCGTTTCTTCCAGGACAGG	5406
Db	4921	GTCTTTGAGTCAGTTTTCAAACCTTGTGGCCTTTGCGTTCCGCCGTTTCTTCCAGGACAGG	4980
Qy	5407	TGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAG	5466
Db	4981	TGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAG	5040
Qy	5467	ATTGAGGTCAATCTGTCGCTGCCCATCAACCCACCATCATCCGTATCATGAGGGTGCTC	5526
Db	5041	ATTGAGGTCAATCTGTCGCTGCCCATCAACCCACCATCATCCGTATCATGAGGGTGCTC	5100
Qy	5527	CGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGCAC	5586
Db	5101	CGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGCAC	5160
Qy	5587	ACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTATTGTTT	5646
Db	5161	ACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTATTGTTT	5220
Qy	5647	TTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACAC	5706
Db	5221	TTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACAC	5280
Qy	5707	CCTTGTGAGGGCTTGGGTGCGGCATGCCACCTTTAGGAACTTTGGTATGGCCTTTCTGACC	5766
Db	5281	CCTTGTGAGGGCTTGGGTGCGGCATGCCACCTTTAGGAACTTTGGTATGGCCTTTCTGACC	5340

Qy	5767	CTCTTCCGAGTCTCCACTGGTGACAACCTGGAATGGTATTATGAAGGACCCCTTCCCGGGAC	5826
Db	5341	CTCTTCCGAGTCTCCACTGGTGACAACCTGGAATGGTATTATGAAGGACCCCTCCGGGAC	5400
Qy	5827	TGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTGTCCTTC	5886
Db	5401	TGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTGTCCTTC	5460
Qy	5887	GTGCTGACGGCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAGCACCTG	5946
Db	5461	GTGCTGACGGCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAGCACCTG	5520
Qy	5947	GAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAG	6006
Db	5521	GAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAG	5580
Qy	6007	ATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCCTTCCTCTGGCCCCGG	6066
Db	5581	ATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCCTTCCTCTGGCCCCGG	5640
Qy	6067	GTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCAC	6126
Db	5641	GTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCAC	5700
Qy	6127	ATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACGATGGTACCCACCCCGAGGAG	6186
Db	5701	ATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACGATGGTACCCACCCCGAGGAG	5760
Qy	6187	GTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGAGCCGGACG	6246
Db	5761	GTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTGAGCCGGACG	5820
Qy	6247	CACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTA	6306
Db	5821	CACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTA	5880
Qy	6307	GGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTTCACTCC	6366
Db	5881	GGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTTCACTCC	5940
Qy	6367	CAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTGCTCCAG	6426
Db	5941	CAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTGCTCCAG	6000
Qy	6427	CCTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGCTCCCCT	6486
Db	6001	CCTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGCTCCCCT	6060
Qy	6487	CTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGCAG	6546
Db	6061	CTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGCAG	6120
Qy	6547	GGCCTGGGTAGCCGGAAGACCTGTTGTGTCAGAGGTGAGTGGGCCCTCCTGCCCTCTGACC	6606
Db	6121	GGCCTGGGTAGCCGGAAGACCTGTTGTGTCAGAGGTGAGTGGGCCCTCCTGCCCTCTGACC	6180
Qy	6607	CGGTCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAG	6666
Db	6181	CGGTCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAG	6240

Art Unit: 1646

```
Qy      6667 AGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCCTTGCCCAGGCCTGGAACCCAGCTGG 6726
      |||
Db      6241 AGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCCTTGCCCAGGCCTGGAACCCAGCTGG 6300

Qy      6727 GCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATT 6786
      |||
Db      6301 GCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATT 6360

Qy      6787 TCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCTGTTCCACGGGACCTGAAGAAG 6846
      |||
Db      6361 TCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCTGTTCCACGGGACCTGAAGAAG 6420

Qy      6847 TGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGATGAACAG 6906
      |||
Db      6421 TGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGATGAACAG 6480

Qy      6907 CGGAGACACTCCATTGCTGTCTGCTGACAGCGGCTCCCAACCCCGCCTATGTCCA 6966
      |||
Db      6481 CGGAGACACTCCATTGCTGTCTGCTGACAGCGGCTCCCAACCCCGCCTATGTCCA 6540

Qy      6967 AGCCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCTGGGAGCCGGCCTAAGAAAAA 7026
      |||
Db      6541 AGCCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCTGGGAGCCGGCCTAAGAAAAA 6600

Qy      7027 CTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCCCCATGC 7086
      |||
Db      6601 CTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCCCCATGC 6660

Qy      7087 AGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCCTCGGTC 7146
      |||
Db      6661 AGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCCTCGGTC 6720

Qy      7147 TCCAGCCCCCTTGACAGCACGGCTGCCTCACCCTCCCCAAAGAAAGACACGCTGAGTCTC 7206
      |||
Db      6721 TCCAGCCCCCTTGACAGCACGGCTGCCTCACCCTCCCCAAAGAAAGACACGCTGAGTCTC 6780

Qy      7207 TCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 7242
      |||
Db      6781 TCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 6816
```

Proteins

Run on: February 9, 2007, 00:38:40 ; Search time 287 Seconds
(without alignments)
3899.322 Million cell updates/sec

Title: US-09-346-794-24

Perfect score: 12028

Sequence: 1 MLPHRVPRCV RTPPLRGSAR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Art Unit: 1646

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*

- 1: geneseq1980s:*
- 2: geneseq1990s:*
- 3: geneseq2000s:*
- 4: geneseq2001s:*
- 5: geneseq2002s:*
- 6: geneseq2003as:*
- 7: geneseq2003bs:*
- 8: geneseq2004s:*
- 9: geneseq2005s:*
- 10: geneseq2006s:*
- 11: geneseq2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB ID	Description
	Score	Match			
1	12028	100.0	2287 4	AAB66475	Aab66475 Rat alpha
2	11657	96.9	2254 2	AAY14590	Aay14590 Rat T-typ
3	11626	96.7	2272 2	AAY14592	Aay14592 Rat T-typ
4	11610.5	96.5	2265 2	AAY14591	Aay14591 Rat T-typ
5	11606.5	96.5	2247 2	AAY14593	Aay14593 Rat T-typ
6	11542.5	96.0	2428 3	AAY70720	Aay70720 Rat pancr
7	10857	90.3	2250 2	AAY14586	Aay14586 Human T-t
8	10838	90.1	2268 9	AEC95659	Aec95659 Calcium c
9	10838	90.1	2268 9	AEE17869	Aee17869 Human T-t
10	10838	90.1	2268 10	AEI99662	Aei99662 Human CCA
11	10833	90.1	2268 2	AAY14588	Aay14588 Human T-t
12	10820.5	90.0	2273 4	AAE01019	Aae01019 Human T-t
13	10810.5	89.9	2261 2	AAY14587	Aay14587 Human T-t
14	10806.5	89.8	2243 2	AAY14589	Aay14589 Human T-t
15	10806.5	89.8	2243 7	ADJ68819	Adj68819 Human hea
16	10732.5	89.2	2377 8	ADQ89064	Adq89064 Human uro
17	10732.5	89.2	2377 10	AEI99755	Aei99755 Human CCA
18	10533	87.6	2266 4	AAB66481	Aab66481 Human alp
19	7274	60.5	1513 9	AEC95660	Aec95660 Calcium c
20	7274	60.5	1513 10	AEI99663	Aei99663 Human CCA
21	7252.5	60.3	1504 10	AEI99760	Aei99760 Human CCA
22	6246	51.9	2359 9	AEC05419	Aec05419 Rat T-typ
23	6243	51.9	2359 9	AEC05417	Aec05417 Rat T-typ
24	6243	51.9	2359 9	AEC05415	Aec05415 Rat T-typ
25	6226.5	51.8	2359 4	AAB66476	Aab66476 Rat alpha
26	6222	51.7	2353 2	AAY06299	Aay06299 Human act
27	6222	51.7	2353 6	ABP72254	Abp72254 Human T-t
28	6222	51.7	2353 7	ADJ69322	Adj69322 Human hea
29	6222	51.7	2353 10	AEI99763	Aei99763 Human CCA

Art Unit: 1646

30	6221	51.7	2353	2	AAY06298	Aay06298 Human act
31	6217	51.7	2347	9	AEC95642	Aec95642 Calcium c
32	6217	51.7	2347	10	AEI99645	Aei99645 Human CCA
33	6195.5	51.5	2353	5	ABG30840	Abg30840 Human vol
34	5872	48.8	1207	4	AAU00474	Aau00474 Human T-t
35	5872	48.8	1207	10	AEK52293	Aek52293 Human T-t
36	5835	48.5	2044	2	AAY14594	Aay14594 Human T-t
37	5827	48.4	2038	2	AAY14595	Aay14595 Human T-t
38	5718.5	47.5	2034	2	AAU06300	Aay06300 Human act
39	5409	45.0	2175	5	AAU10535	Aau10535 Human T-t
40	5409	45.0	2175	6	ABU08511	Abu08511 Human T-t
41	5409	45.0	2175	8	ADH69265	Adh69265 Human TCC
42	5405.5	44.9	2188	5	AAU10536	Aau10536 Human T-t
43	5405.5	44.9	2188	6	ABU08512	Abu08512 Human T-t
44	5405.5	44.9	2188	8	ADH69267	Adh69267 Human TCC
45	5361.5	44.6	1981	9	ADZ58492	Adz58492 Human alp

ALIGNMENTS

RESULT 2

AAY14590

ID AAY14590 standard; protein; 2254 AA.

XX

AC AAY14590;

XX

DT 07-DEC-1999 (first entry)

XX

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1a).

XX

KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
 KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.

XX

OS Rattus sp.

XX

PN WO9929847-A1.

XX

PD 17-JUN-1999.

XX

PF 30-OCT-1998; 98WO-US023161.

XX

PR 05-DEC-1997; 97US-00985809.

XX

PA (LOYO) UNIV LOYOLA CHICAGO.

XX

PI Perez-Reyes E, Cribbs LL;

XX

DR WPI; 1999-394972/33.

DR

N-PSDB; AAX83485.

XX

PT New T-type voltage-gated calcium channels.

XX

PS Disclosure; Page 67-76; 138pp; English.

XX

CC This sequence represents a rat T-type voltage-gated calcium (Ca) channel

alpha-1-G designated rCavT1a. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

Sequence 2254 AA;

Query Match 96.9%; Score 11657; DB 2; Length 2254;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2219; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	62	GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERVSM	121
Db	30	GRQGPSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERVSM	89
Qy	122	VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG	181
Db	90	VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG	149
Qy	182	DTWNRLDFFIIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLD	241
Db	150	DTWNRLDFFIIVIAAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLD	209
Qy	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQTENEDES	301
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQTENEDES	269
Qy	302	ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNC	361
Db	270	ICSQPRENGMRSCRSVPTLRGEGGGPPCSLDYETYNSSSNTTCVNWNQYYTNC	329
Qy	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGS	421
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGS	389
Qy	422	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYL	481
Db	390	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYL	449
Qy	482	RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSTRSHRRLSVHHLVHHHHHHHHYHLGN	541
Db	450	RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSTRSHRRLSVHHLVHHHHHHHHYHLGN	509
Qy	542	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAEVSHSFYHADCHLEP	601
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAEVSHSFYHADCHLEP	569
Qy	602	APPPRCPSEASGRITVSGSKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSENI	661

Art Unit: 1646

Db 570 APPPRCPSEASGRVTGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSTFNIPPGPF 629

Qy 662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721

Db 630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy 722 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 781

Db 690 SEAVYEFTQDAQHSDLRDPHSRRRQSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMMLKLLVYGPFYIKNPYN 841

Db 750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMMLKLLVYGPFYIKNPYN 809

Qy 842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRFPLALQRLVVLMTMDNVATF 901

Db 810 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRFPLALQRLVVLMTMDNVATF 869

Qy 902 CMLMLFIFIFISILGMHLFGCKFASERDGD TLPDRKNFDSLLWAI VTFQILTQEDWNKV 961

Db 870 CMLMLFIFIFISILGMHLFGCKFASERDGD TLPDRKNFDSLLWAI VTFQILTQEDWNKV 929

Qy 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEP DFFSPSVD 1021

Db 930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEP DFFSPSVD 989

Qy 1022 GDGDRKKRLALVALGEHAELRKSLPPLI IHTAATPM SHPKSSSTGVGEALGSGSRRTSS 1081

Db 990 GDGDRKKRLALVALGEHAELRKSLPPLI IHTAATPM SHPKSSSTGVGEALGSGSRRTSS 1049

Qy 1082 SGSAEPGA AHHEMKCPP SARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141

Db 1050 SGSAEPGA AHHEMKCPP SARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1109

Qy 1142 LLSGEGQESQDEEESSEEDRAS PAGSDHRH RGS LEREAKSSFDLPDTLQVPGLHRTASGR 1201

Db 1110 LLSGEGQESQDEEESSEEDRAS PAGSDHRH RGS LEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy 1202 SSASEHQDCNGKSASGRLARTLR TDDPQLDGD DDND EGNLSKGERIQA WVR SRLPACCRE 1261

Db 1170 SSASEHQDCNGKSASGRLARTLR TDDPQLDGD DDND EGNLSKGERIQA WVR SRLPACCRE 1229

Qy 1262 RDSWSAYIFPPQSRFRLLCHRIITHKMF DHVVLV IIFLNCITIAMERPKIDPHSAERIFL 1321

Db 1230 RDSWSAYIFPPQSRFRLLCHRIITHKMF DHVVLV IIFLNCITIAMERPKIDPHSAERIFL 1289

Qy 1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLV LISVIDILVSMVSDSG 1381

Db 1290 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLV LISVIDILVSMVSDSG 1349

Qy 1382 TKILGMLRVLRLRLR LRLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICAFFIIFGILG 1441

Db 1350 TKILGMLRVLRLRLR LRLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICAFFIIFGILG 1409

Qy 1442 VQLFKGKFFVCQGEDTRNITNKSDCAEAS YRVRHKYNFDNLGQALMSL FVLASKDGWVD 1501

Db 1410 VQLFKGKFFVCQGEDTRNITNKSDCAEAS YRVRHKYNFDNLGQALMSL FVLASKDGWVD 1469

Qy 1502 IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFL LIVAFFVLNMFVGVVVENFHKCRQH QEEE 1561

Art Unit: 1646

```
Db      1470  |||IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQQEEE 1529
Qy      1562  EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSYRFRLLVHHLCTSHYLDLFIITGVI 1621
Db      1530  |||EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSYRFRLLVHHLCTSHYLDLFIITGVI 1589
Qy      1622  GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAPRRFFQDRWNQLDLA 1681
Db      1590  |||GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAPRRFFQDRWNQLDLA 1649
Qy      1682  IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMALLHTVMQALP 1741
Db      1650  |||IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMALLHTVMQALP 1709
Qy      1742  QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTTLFRVSTG 1801
Db      1710  |||QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTTLFRVSTG 1769
Qy      1802  DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMKHLEESNKEA 1861
Db      1770  |||DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVNVIIVLMKHLEESNKEA 1829
Qy      1862  KEEAELEAELELEMTLSLPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
Db      1830  |||KEEAELEAELELEMTLSLPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1889
Qy      1922  SLEHPTMPHPPEEVPVPLGPDLLTVRKSQVSRTHSLPNDSYMCRNGSTAERSLGHARGWGL 1981
Db      1890  |||SLEHPTMPHPPEEVPVPLGPDLLTVRKSQVSRTHSLPNDSYMCRNGSTAERSLGHARGWGL 1949
Qy      1982  PKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2041
Db      1950  |||PKAQSGSILSVHSQPADTSCILQPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2009
Qy      2042  RQAAIRTDSDLVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101
Db      2010  |||RQAAIRTDSDLVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2069
Qy      2102  RLPAPCPGLEPSWAKDPPETRSSLLELDTLSWISGDLPLSSQEEPLFPRDLKKCYSVETQ 2161
Db      2070  |||RLPAPCPGLEPSWAKDPPETRSSLLELDTLSWISGDLPLSSQEEPLFPRDLKKCYSVETQ 2129
Qy      2162  SCRRLPGFWLDEQRRHSIAVSCLDGSGPRLCPSPSSLGGQPLGGPGSRPKKLSPPSIS 2221
Db      2130  |||SCRRLPGFWLDEQRRHSIAVSCLDGSGPRLCPSPSSLGGQPLGGPGSRPKKLSPPSIS 2189
Qy      2222  IDPPESQGSRRPPCSPGVCLRRRAPASDSKDPVSSPLDSTAASPSPKDTLSLSGLSSDP 2281
Db      2190  |||IDPPESQGSRRPPCSPGVCLRRRAPASDSKDPVSSPLDSTAASPSPKDTLSLSGLSSDP 2249
Qy      2282  TDMDP 2286
Db      2250  |||TDMDP 2254
```

RESULT 3

AAY14592

ID AAY14592 standard; protein; 2272 AA.

XX

Art Unit: 1646

Db 90 VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy 182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTP 241
|||||

Db 150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDTP 209

Qy 242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQTENEDES PF 301
|||||

Db 210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQTENEDES PF 269

Qy 302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNC SAGEHN 361
|||||

Db 270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNC SAGEHN 329

Qy 362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
|||||

Db 330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy 422 CLVVIATQFSETKQRESQLMREQRVRLSNASTLASFSEPGSCYEELLKYLVIYILRKAAR 481
|||||

Db 390 CLVVIATQFSETKQRESQLMREQRVRLSNASTLASFSEPGSCYEELLKYLVIYILRKAAR 449

Qy 482 RLAQVSRAIGVRAGLLSSPVARSQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 541
|||||

Db 450 RLAQVSRAIGVRAGLLSSPVARSQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 509

Qy 542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
|||||

Db 510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

Qy 602 APPPRCPSEASGRTVSGSKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSTFNI PP GPF 661
|||||

Db 570 APPPRCPSEASGRTVSGSKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSTFNI PP GPF 629

Qy 662 SSMHKLETTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 721
|||||

Db 630 SSMHKLETTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPSD 689

Qy 722 SEAVYEFTQDAQHSDLRDPHSRRRQRLSGPDAEPSSVLAFWRLICDTRKIVDSKYFGRG 781
|||||

Db 690 SEAVYEFTQDAQHSDLRDPHSRRRQRLSGPDAEPSSVLAFWRLICDTRKIVDSKYFGRG 749

Qy 782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFYIKNPYN 841
|||||

Db 750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFYIKNPYN 809

Qy 842 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRFPLALQRLVVLTKTMDNVATF 901
|||||

Db 810 IFDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVRFPLALQRLVVLTKTMDNVATF 869

Qy 902 CMLLMFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAI VTFQILTQEDWNKV 961
|||||

Db 870 CMLLMFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAI VTFQILTQEDWNKV 929

Qy 962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEP DFFSPSVD 1021
|||||

Db 930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEP DFFSPSVD 989

Qy 1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPM SHPKSSSTGVGEALGSGSRTSS 1081
|||||

Art Unit: 1646

Db 990 GDGDRKKRLALVALGEHAELRKSLPLIIHTAATPM SHPKSSSTGVGEALGSGSRRTSS 1049

Qy 1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
|||||

Db 1050 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1109

Qy 1142 LLSGEGQESQDEEESSEEDRASPGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
|||||

Db 1110 LLSGEGQESQDEEESSEEDRASPGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy 1202 SSASEHQDCNGKSASGR LARTLR TDDPQLDGD DDDNDEGNLSKGERIQAWVRSLPACCRE 1261
|||||

Db 1170 SSASEHQDCNGKSASGR LARTLR TDDPQLDGD DDDNDEGNLSKGERIQAWVRSLPACCRE 1229

Qy 1262 RDSWSAYIFPPQSRFRL LCHRIITHKMF DHVVLVII FLNCITIAMERPKIDPHSAERIFL 1321
|||||

Db 1230 RDSWSAYIFPPQSRFRL LCHRIITHKMF DHVVLVII FLNCITIAMERPKIDPHSAERIFL 1289

Qy 1322 TLSNYIFTAVFLAEMTVK VVALGWCFGEQAYLRSSWNVLDGLLV LISVIDILVSMVSDSG 1381
|||||

Db 1290 TLSNYIFTAVFLAEMTVK VVALGWCFGEQAYLRSSWNVLDGLLV LISVIDILVSMVSDSG 1349

Qy 1382 TKILGMLRVLRLRLR TLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
|||||

Db 1350 TKILGMLRVLRLRLR TLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409

Qy 1442 VQLFKGKFFVCQGEDTRNITNKSDCAEAS YRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
|||||

Db 1410 VQLFKGKFFVCQGEDTRNITNKSDCAEAS YRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1469

Qy 1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
|||||

Db 1470 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1529

Qy 1562 EARRREEKRLRRLEKKRRSKEKQMA-----EAQCKPYYS DYSRFRLL 1603
|||||

Db 1530 EARRREEKRLRRLEKKRRSKEKQMA DMLDDVIASGSSASAASEAQCKPYYS DYSRFRLL 1589

Qy 1604 VHHLCTSHYLDL FITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLV 1663
|||||

Db 1590 VHHLCTSHYLDL FITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLV 1649

Qy 1664 AFAFRFFQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLL 1723
||

Db 1650 AFGFRFFQDRWNQDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLL 1709

Qy 1724 KMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHA 1783
|||||

Db 1710 KMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHA 1769

Qy 1784 TFRNFGMAFLT LFRVSTGDNWNGIMKDP SRDCDQESTCYNTVISPIYFVSFVLTAQFVLV 1843
|||||

Db 1770 TFRNFGMAFLT LFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLV 1829

Qy 1844 NVVIAVLMKHLEESNKEAKEEAELEAELEEMKTLSPQPHSPLGSPFLWPGVEGVNSTDS 1903
|||||

Db 1830 NVVIAVLMKHLEESNKEAKEEAELEAELEEMKTLSPQPHSPLGSPFLWPGVEGVNSTDS 1889

Qy 1904 PKPGAPHTTAHIGAASGFSLEHPTMVPHP EEPVPLGPDLLTVRKSGVSRTHSLPNDSYM 1963
|||||

Art Unit: 1646

Db 1890 PKPGAPHTTAHIGAASGFSLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYM 1949

Qy 1964 CRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGA 2023
|||||

Db 1950 CRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGA 2009

Qy 2024 IPKLPPPGRSPLAQRPLRRQAAIRTDSDLVQGLGSREDLLSEVSGPSCPLTRSSSFWGGG 2083
|||||

Db 2010 IPKLPPPGRSPLAQRPLRRQAAIRTDSDLVQGLGSREDLLSEVSGPSCPLTRSSSFWGGG 2069

Qy 2084 SIQVQQRSIGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLSSQ 2143
|||||

Db 2070 SIQVQQRSIGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLPLSSQ 2129

Qy 2144 EEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSSLGGQP 2203
|||||

Db 2130 EEPLFPRDLKNCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSPSSLGGQP 2189

Qy 2204 LGGPGSRPKKLSPPSISIDPPESQGSRRPPSPGVCLRRRAPASDSKDPSVSSPLDSTAA 2263
|||||

Db 2190 LGGPGSRPKKLSPPSISIDPPESQGSRRPPSPGVCLRRRAPASDSKDPSVSSPLDSTAA 2249

Qy 2264 SPSPKKDTLSLSGLSSDPTDMDP 2286
|||||

Db 2250 SPSPKKDTLSLSGLSSDPTDMDP 2272

RESULT 4

AAY14591

ID AAY14591 standard; protein; 2265 AA.

XX

AC AAY14591;

XX

DT 07-DEC-1999 (first entry)

XX

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1b).

XX

KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy.

XX

OS Rattus sp.

XX

PN WO9929847-A1.

XX

PD 17-JUN-1999.

XX

PF 30-OCT-1998; 98WO-US023161.

XX

PR 05-DEC-1997; 97US-00985809.

XX

PA (LOYO) UNIV LOYOLA CHICAGO.

XX

PI Perez-Reyes E, Cribbs LL;

XX

DR WPI; 1999-394972/33.

DR N-PSDB; AAX83486.

XX

PT New T-type voltage-gated calcium channels.

XX

PS Disclosure; Page 76-85; 138pp; English.

Art Unit: 1646

XX
CC This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC alpha-1-G designated rCavT1b. Voltage gated channels are membrane bound
CC glycosylated proteins formed of several subunits. The large alpha
CC subunits form a pore in the membrane that is selective for a given ionic
CC species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC -type Ca channels are activated at a lower voltage than L- or N-type
CC channels. Characteristics of T-type channels include short current time,
CC slow activation kinetics near threshold, fast inactivation kinetics and
CC slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC -channels contains a putative IVS4 region comprising the amino acid
CC sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC channel proteins can be used to screen for drugs which affect calcium
CC channels. Methods are also disclosed for treating a disease or disorder
CC associated with a deficiency in a native T-type calcium channel nucleic
CC acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX
SQ Sequence 2265 AA;

Query Match 96.5%; Score 11610.5; DB 2; Length 2265;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2213; Conservative 1; Mismatches 11; Indels 11; Gaps 1;

Qy	62	GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERSVMSL	121
Db	30	GRQGPSTKDPGSADSEAEGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERSVMSL	89
Qy	122	VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG	181
Db	90	VILLNCVTLMGFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG	149
Qy	182	DTWNRLDFFIIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDITLP	241
Db	150	DTWNRLDFFIIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLDITLP	209
Qy	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQTENEDESFF	301
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQTENEDESFF	269
Qy	302	ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNC SAGEHN	361
Db	270	ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNC SAGEHN	329
Qy	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIIYFILLIIVGSFFMINL	421
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIIYFILLIIVGSFFMINL	389
Qy	422	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIYLKAAAR	481
Db	390	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIYLKAAAR	449
Qy	482	RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN	541
Db	450	RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN	509
Qy	542	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ	601
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ	569

Qy	602	APPPRCPSEASGRTVSGSGKYPTVHTSPPPPEILKDKALVEVAPSPGPPTLTLSFNIPPGPF	661
Db	570	APPPRCPSEASGRTVSGSGKYPTVHTSPPPPEILKDKALVEVAPSPGPPTLTLSFNIPPGPF	629
Qy	662	SSMHKLELTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD	721
Db	630	SSMHKLELTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD	689
Qy	722	SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG	781
Db	690	SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG	749
Qy	782	IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPGFYIKNPYN	841
Db	750	IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPGFYIKNPYN	809
Qy	842	IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFPLALQRQLVVLMTMDNVATF	901
Db	810	IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFPLALQRQLVVLMTMDNVATF	869
Qy	902	CMLMLLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTVFQILTQEDWNKV	961
Db	870	CMLMLLFIFIFSILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTVFQILTQEDWNKV	929
Qy	962	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDDFFSPSVD	1021
Db	930	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDDFFSPSVD	989
Qy	1022	GDGDRKKRLALVALGEHAELRKSLPLLIHTAATPMShPKSSSTGVGEALGSGSRRTSS	1081
Db	990	GDGDRKKRLALVALGEHAELRKSLPLLIHTAATPMShPKSSSTGVGEALGSGSRRTSS	1049
Qy	1082	SGSAEPGAHHHEMKPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS	1141
Db	1050	SGSAEPGAHHHEMKPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS	1109
Qy	1142	LLSGEGQESQDEEESSEEDRASPGSDHRHRGSLEREAKSSFDLPDTLQVPLHRTASGR	1201
Db	1110	LLSGEGQESQDEEESSEEDRASPGSDHRHRGSLEREAKSSFDLPDTLQVPLHRTASGR	1169
Qy	1202	SSASEHQDCNGKSASGRLARTLRITDDPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRE	1261
Db	1170	SSASEHQDCNGKSASGRLARTLRITDDPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRE	1229
Qy	1262	RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFL	1321
Db	1230	RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFL	1289
Qy	1322	TLSNYIFTAVFLAEMTVKVVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG	1381
Db	1290	TLSNYIFTAVFLAEMTVKVVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG	1349
Qy	1382	TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICAFFIIFGILG	1441
Db	1350	TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICAFFIIFGILG	1409
Qy	1442	VQLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKYNFDNLGQALMSLFLVASKDGWVD	1501
Db	1410	VQLFKGKFFVCQGEDTRNITNKSDCAEASRWVRHKYNFDNLGQALMSLFLVASKDGWVD	1469

Qy	1502	IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFFVLNMFVGVVVVENFHKCRQHQEEE	1561
Db	1470	IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFFVLNMFVGVVVVENFHKCRQHQEEE	1529
Qy	1562	EARRREEKRLRRLEKKRR-----SKEKQMAEAQCKPYYSYDSRFRLLVHHLCTS	1610
Db	1530	EARRREEKRLRRLEKKRRNLMLDDVIASGSSASAASEAQCKPYYSYDSRFRLLVHHLCTS	1589
Qy	1611	HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVI FVFESVFKLVAFAFRRF	1670
Db	1590	HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVI FVFESVFKLVAFAGFRRF	1649
Qy	1671	FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRAVLKLLKMAVGMR	1730
Db	1650	FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRAVLKLLKMAVGMR	1709
Qy	1731	ALLHTVMQALPQVGNLGLLFMLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM	1790
Db	1710	ALLHTVMQALPQVGNLGLLFMLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM	1769
Qy	1791	AFLTFRVSTGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVL	1850
Db	1770	AFLTFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVL	1829
Qy	1851	MKHLEESNKEAKEEAELEAELEEMKTLSPQPHSPLGSPFLWPGEVGNSTDSPKPGAPH	1910
Db	1830	MKHLEESNKEAKEEAELEAELEEMKTLSPQPHSPLGSPFLWPGEVGNSTDSPKPGAPH	1889
Qy	1911	TTAHIGAASGFSLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCNRGSTA	1970
Db	1890	TTAHIGAASGFSLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCNRGSTA	1949
Qy	1971	ERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPP	2030
Db	1950	ERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPP	2009
Qy	2031	GRSPLAQRLRRQAAIRTDSDLVQGLSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQR	2090
Db	2010	GRSPLAQRLRRQAAIRTDSDLVQGLSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQR	2069
Qy	2091	SGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLLPSSQEEPLFPR	2150
Db	2070	SGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTLSWISGDLLPSSQEEPLFPR	2129
Qy	2151	DLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGQPLGGPGSR	2210
Db	2130	DLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGQPLGGPGSR	2189
Qy	2211	PKKKLSPPSISIDPPESQSGSRPPCSPGVCLRRRAPASDSKDPVS SPLDSTAASPSPKKD	2270
Db	2190	PKKKLSPPSISIDPPESQSGSRPPCSPGVCLRRRAPASDSKDPVS SPLDSTAASPSPKKD	2249
Qy	2271	TLSLSGLSSDPTDMDP	2286
Db	2250	TLSLSGLSSDPTDMDP	2265

```

ID  AAY14593 standard; protein; 2247 AA.
XX
AC  AAY14593;
XX
DT  07-DEC-1999 (first entry)
XX
DE  Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1d).
XX
KW  Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW  activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS  Rattus sp.
XX
PN  WO9929847-A1.
XX
PD  17-JUN-1999.
XX
PF  30-OCT-1998; 98WO-US023161.
XX
PR  05-DEC-1997; 97US-00985809.
XX
PA  (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI  Perez-Reyes E, Cribbs LL;
XX
DR  WPI; 1999-394972/33.
DR  N-PSDB; AAX83488.
XX
PT  New T-type voltage-gated calcium channels.
XX
PS  Disclosure; Page 94-103; 138pp; English.
XX
CC  This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC  alpha-1-G designated rCavT1d. Voltage gated channels are membrane bound
CC  glycosylated proteins formed of several subunits. The large alpha
CC  subunits form a pore in the membrane that is selective for a given ionic
CC  species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC  each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC  -type Ca channels are activated at a lower voltage than L- or N-type
CC  channels. Characteristics of T-type channels include short current time,
CC  slow activation kinetics near threshold, fast inactivation kinetics and
CC  slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC  voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC  -channels contains a putative IVS4 region comprising the amino acid
CC  sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC  channel proteins can be used to screen for drugs which affect calcium
CC  channels. Methods are also disclosed for treating a disease or disorder
CC  associated with a deficiency in a native T-type calcium channel nucleic
CC  acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ  Sequence 2247 AA;

Query Match          96.5%; Score 11606.5; DB 2; Length 2247;
                      Best Local Similarity 99.4%; Pred. No. 0;
Matches 2211; Conservative 1; Mismatches 6; Indels 7; Gaps 1;

Qy  62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERSML 121
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  30 GROGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERSML 89

```


Qy	1022	GDGDRKKRLALVALGEHAELRKSLLPPLI IHTAATPMSPKSSSTGVGEALGSGSRRTSS	1081
Db	990	GDGDRKKRLALVALGEHAELRKSLLPPLI IHTAATPMSPKSSSTGVGEALGSGSRRTSS	1049
Qy	1082	SGSAEPGAAHHMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS	1141
Db	1050	SGSAEPGAAHHMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS	1109
Qy	1142	LLSGEGQESQDEEESSEEDRASPAAGSDHRHGRSLEREAKSSFDLPDTLQVPGLHRTASGR	1201
Db	1110	LLSGEGQESQDEEESSEEDRASPAAGSDHRHGRSLEREAKSSFDLPDTLQVPGLHRTASGR	1169
Qy	1202	SSASEHQDCNGKSASGRLARTLRITDDPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRE	1261
Db	1170	SSASEHQDCNGKSASGRLARTLRITDDPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRE	1229
Qy	1262	RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIIIFLNCITIAMERPKIDPHSAERIFL	1321
Db	1230	RDSWSAYIFPPQSRFRLLCHRIITHKMFHDVVLVIIIFLNCITIAMERPKIDPHSAERIFL	1289
Qy	1322	TLSNYIFTAVFLAEMTVKVVVALGWCFGEQAYLRSSWNVDGLLVLSIVIDILVSMVSDSG	1381
Db	1290	TLSNYIFTAVFLAEMTVKVVVALGWCFGEQAYLRSSWNVDGLLVLSIVIDILVSMVSDSG	1349
Qy	1382	TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICAFFIIFGILG	1441
Db	1350	TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICAFFIIFGILG	1409
Qy	1442	VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD	1501
Db	1410	VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD	1469
Qy	1502	IMYDGLDAVGVDQQPI MNHNPWMLLYFISFLLIVAFFVLNMFGVVVENFHKCRQHQEEE	1561
Db	1470	IMYDGLDAVGVDQQPI MNHNPWMLLYFISFLLIVAFFVLNMFGVVVENFHKCRQHQEEE	1529
Qy	1562	EARRREEKRLRRLEKKRRSKEQMAEAQCKPYYSYSRFRLLVHHLCTSHYLDLFIITGVI	1621
Db	1530	EARRREEKRLRRLEKKRR-----KAQCKPYYSYSRFRLLVHHLCTSHYLDLFIITGVI	1582
Qy	1622	GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFARFRFFQDRWNQLDLA	1681
Db	1583	GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFARFRFFQDRWNQLDLA	1642
Qy	1682	IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRVLKLLKMAVGMRALLHTVMQALP	1741
Db	1643	IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRVLKLLKMAVGMRALLHTVMQALP	1702
Qy	1742	QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTFRVSTG	1801
Db	1703	QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTFRVSTG	1762
Qy	1802	DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVIIVLMKHLEESNKEA	1861
Db	1763	DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVIIVLMKHLEESNKEA	1822
Qy	1862	KEEAELAELELEMKTLSPOPHSPPLGSPFLWPGEVGNSTDSPKPGAPHTTAHIGAASGF	1921
Db	1823	KEEAELAELELEMKTLSPOPHSPPLGSPFLWPGEVGNSTDSPKPGAPHTTAHIGAASGF	1882

Art Unit: 1646

Qy	1922	SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL	1981
Db	1883	SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL	1942
Qy	1982	PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAI PKLPPPGRSPLAQRPLR	2041
Db	1943	PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAI PKLPPPGRSPLAQRPLR	2002
Qy	2042	RQAAIRTDSDLVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI	2101
Db	2003	RQAAIRTDSDLVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI	2062
Qy	2102	RLPAPCPGLEPSWAKDPPETRSSLLELDTLSWISGDLPLSSQEEPLFPRDLKKCYSVETQ	2161
Db	2063	RLPAPCPGLEPSWAKDPPETRSSLLELDTLSWISGDLPLSSQEEPLFPRDLKKCYSVETQ	2122
Qy	2162	SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS	2221
Db	2123	SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS	2182
Qy	2222	IDPPESQGSRRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKDTLSLSGLSSDP	2281
Db	2183	IDPPESQGSRRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKDTLSLSGLSSDP	2242
Qy	2282	TDMDP	2286
Db	2243	TDMDP	2247

Art Unit: 1646

Appendix B

Database search of nucleic acid and polypeptide sequence with the greatest identity to SEQ ID NO :23 and SEQ ID NO:24 are provided below. A comparison of the sequences disclosed by Perez-Reyes, W. (Nature, Vol. 391, pages 900,1998) that have greatest identity with SEQ ID NO :23 and SEQ ID NO:24 are provided in detail.

Run on: February 9, 2007, 10:42:19 ; Search time 44042 Seconds
(without alignments)
11833.410 Million cell updates/sec

Title: US-09-346-794-23
Perfect score: 7540
Sequence: 1 ccgtctctggcgcggagcgg.....acgtttgtgcagaatctcta 7540

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Art Unit: 1646

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	7540	100.0	7540	2	AX068898	AX068898 Sequence
2	7510.4	99.6	7542	6	RNCAA1G	AF027984 Rattus no
3	6956.4	92.3	7286	6	AF125161	AF125161 Rattus no
4	6955.4	92.2	7285	2	BD224079	BD224079 T-type ca
5	6910.4	91.6	6942	6	AF290212	AF290212 Rattus no
6	6816.6	90.4	7129	2	BD224078	BD224078 T-type ca
7	6607.2	87.6	7527	6	BC057399	BC057399 Mus muscu
8	6492.2	86.1	7281	6	DQ317412	DQ317412 Mus muscu
9	6401	84.9	7625	6	MMU012569	AJ012569 Mus muscu
10	5810.6	77.1	7741	2	BD407048	BD407048 DNA ENCOD
11	5810.6	77.1	7741	2	AR201015	AR201015 Sequence
12	5758.6	76.4	7512	5	BC110995	BC110995 Homo sapi
13	5737.2	76.1	7349	5	AF190860	AF190860 Homo sapi
14	5714.8	75.8	7274	5	AF126966	AF126966 Homo sapi
15	5664.4	75.1	7253	5	AF126965	AF126965 Homo sapi
16	5507.8	73.0	6768	5	DQ494455	DQ494455 Homo sapi
17	5457.4	72.4	6747	5	DQ494450	DQ494450 Homo sapi
18	5444	72.2	6801	5	DQ494453	DQ494453 Homo sapi
19	5436.6	72.1	6786	5	AF227747	AF227747 Homo sapi
20	5428.8	72.0	6837	5	DQ494468	DQ494468 Homo sapi
21	5421.4	71.9	6822	5	AF227744	AF227744 Homo sapi
22	5419.8	71.9	6822	2	BD407047	BD407047 DNA ENCOD
23	5419.8	71.9	6822	2	AR201014	AR201014 Sequence
24	5399	71.6	7825	2	DD222996	DD222996 Genes for
25	5378.4	71.3	6816	5	DQ494459	DQ494459 Homo sapi
26	5371	71.2	6801	5	AF227751	AF227751 Homo sapi
27	5365	71.2	6870	5	DQ494464	DQ494464 Homo sapi
28	5364.8	71.2	6891	5	DQ494471	DQ494471 Homo sapi
29	5364.8	71.2	6912	5	DQ494456	DQ494456 Homo sapi
30	5357.6	71.1	6855	5	AF227749	AF227749 Homo sapi
31	5357.4	71.1	6897	5	AF227746	AF227746 Homo sapi
32	5351	71.0	6698	5	DQ494449	DQ494449 Homo sapi
33	5337.6	70.8	6752	5	DQ494452	DQ494452 Homo sapi
34	5326.4	70.6	6795	5	DQ494457	DQ494457 Homo sapi
35	5322.4	70.6	6788	5	DQ494466	DQ494466 Homo sapi
36	5313	70.5	6849	5	DQ494461	DQ494461 Homo sapi
37	5303	70.3	6921	5	AF227748	AF227748 Homo sapi
38	5295.6	70.2	6731	5	DQ494451	DQ494451 Homo sapi
39	5285.8	70.1	6981	5	DQ494469	DQ494469 Homo sapi
40	5278.4	70.0	6966	5	AF227745	AF227745 Homo sapi
41	5275.2	70.0	6762	5	DQ494477	DQ494477 Homo sapi
42	5272	69.9	6767	5	DQ494458	DQ494458 Homo sapi
43	5263.2	69.8	6756	5	DQ494478	DQ494478 Homo sapi
44	5258.6	69.7	6821	5	DQ494462	DQ494462 Homo sapi
45	5238	69.5	6699	5	DQ494472	DQ494472 Homo sapi

ALIGNMENTS

Art Unit: 1646

RESULT 2

RNCAA1G

LOCUS RNCAA1G 7542 bp mRNA linear ROD 24-OCT-1998

DEFINITION Rattus norvegicus low voltage-activated, T-type calcium channel
alpha subunit (CACNA1G) mRNA, complete cds.

ACCESSION AF027984

VERSION AF027984.1 GI:3786350

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 7542)

AUTHORS Perez-Reyes, E., Cribbs, L.L., Daud, A., Lacerda, A.E., Barclay, J.,
Williamson, M.P., Fox, M., Rees, M. and Lee, J.H.TITLE Molecular characterization of a neuronal low-voltage-activated
T-type calcium channel

JOURNAL Nature 391 (6670), 896-900 (1998)

PUBMED 9495342

REFERENCE 2 (bases 1 to 7542)

AUTHORS Cribbs, L.L., Yang, J., Daud, A., Lee, J.-H. and Perez-Reyes, E.

TITLE Direct Submission

JOURNAL Submitted (02-OCT-1997) Physiology, Loyola University Medical
Center, 2160 South First Avenue, Maywood, IL 60153, USA

REFERENCE 3 (bases 1 to 7542)

AUTHORS Cribbs, L.L., Yang, J., Daud, A., Lee, J.-H. and Perez-Reyes, E.

TITLE Direct Submission

JOURNAL Submitted (22-OCT-1998) Physiology, Loyola University Medical
Center, 2160 South First Avenue, Maywood, IL 60153, USA

REMARK Sequence update by submitter

COMMENT On Oct 24, 1998 this sequence version replaced gi:2921748.

FEATURES Location/Qualifiers

source

1. .7542
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/chromosome="17"
/map="17; between AFMA126YD5 and D17S798"
/tissue_type="brain"
/clone_lib="Clontech catalog number RL3005a"

gene

1. .7542
/gene="CACNA1G"

CDS

483. .7247
/gene="CACNA1G"
/note="similar to Caenorhabditis elegans C54D2.5 protein
encoded by the sequence presented in GenBank Accession
Number U37548; alpha-1G calcium channel alpha subunit"
/codon_start=1
/product="low voltage-activated, T-type calcium channel
alpha subunit"
/protein_id="AAC67372.1"
/db_xref="GI:3786351"
/translation="MDEEDGAGAEESGQPRSFTQLNDLSGAGGRQGPSTKDPGSA
DSEAEGLPYPALAPVFFYLSQDSRPRSWCLRTVCNPWFERSMLVILLNCVTLGMFR
PCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIV
IAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLTLLDTPMLGNVLLLC
FFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQTENEDESPFICSQPRE

Art Unit: 1646

NGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNC SAGEHNPFGKA
 INFNDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFYIFILLIIVGSFFMINLCLV
 VIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIILRKAARR
 LAQVSRAGVVRAGLLSSPVARSGQEPQPSGSTRSHRRLSVHHLVHHHHHHHHYHLG
 NGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPV
 RCQAPPPRCPSEASGRTVGSQKVYPTVHTSPPEILKDKALVEVAPSPGPPTLTSFNI
 PPGPFSSMHKLETTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESAD
 HVMPSDSDSEAVYEFTQDAQHSDLRDPHSRRRQSRSLGPDAPSSSVLAFWRLICDTRFKI
 VDSKYFGRGIMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVLV
 GPFYIKNPYNI FDGVIVVISVWEIVGQGGGLSVLRTFRLMRVLKLVFLPALQRQL
 VVLMKTMNDVATFCMLLMLFIFIFISILGMHLFGCKFASERDGTLPDRKNFDSLWAI
 VTVFQILTQEDWNKVLNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFAEG
 DATKSESEPDFSPSPVDGDRKKRLALVALGEHAELRKSLLPPLIHTAATPMSHPK
 SSSTGVGEALGSGSRRTSSSGSAEPGAHHHEMKCPPSARSSPHSPWSAASWTSSRSS
 RNSLGRAPSLKRRSPSGERRSLLSGEGQESQDEEESSEEDRASPGSDHRHRSGLERE
 AKSSFDLPDTLQVPLHRTASGRSSASEHQDCNGKSASGRRLARTLRDTPQLDGGDDN
 DEGNLSKGERIQAWVRSLPACCRERDSWSAYIFPPQSRFRLCHRIITHKMFHDHVV
 VIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLAEMTVKVVALGWCFCGEQAY
 LRSSWNVDGLLVLSVIDILVSMVSDSGTKILGMLRVLRLLRTLRLPLRVISRAQGLK
 LVVETLMSSLKPIGNIVVICCAFFIIFGILGVQLFKGKFVFCQGEDTRNITNKSDCAE
 ASYRWVRHKYNFDNLGQALMSLFVLASKDGWVDIMYDGLDAVGVDQQPMNHNPNWMLL
 YFISFLLIVAFFVLNMFVGVVVENFHKCRQHQQEEEEARRREEKRLRRLKEKKRSKEKQ
 MAEAQCKPYSDYSRFRLLVHHLCTSHYLDLFTIGVIGLNVVTMAMEHYQQPQILDEA
 LKICNYIFTVIFVFESVFKLVAFGFRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLS
 LPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLHTVMQALPQVGNLGLLFFLFFIFA
 ALGVELFGDLECDETHPCPEGLGRHATFRNFGMAFLTFRVSTGDNWNGIMKDTLRDCD
 QESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEAKEEAELEAELELE
 MKTSLSPQPHSPLGSPFLWPVGVEGVNSTDSPKPGAPHTTAHIGAASGFSLEHPTMVPHP
 EEVPPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGLPKAQSGSIL
 SVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAART
 DSLDVQGLGSREDLLSEVSGPSCPLTRSSSFVGGSSIQVQQRSGIQSKVSKHIRLPAP
 CPGLEPSWAKDPPETRSSLLELDTLSWISGDLPLSSQEEPLFPRDLKKCYSVETQSCR
 RRPGFWLDEQRRHSIAVSCLDGSGQPRLCPSSSLGGQPLGGPGSRPKKLSPPSISI
 DPPESQGSRRPPCSPGVCLRRRAPASDSKDPVSSPLDSTAASPSPKDITLSLGLSSD
 PTMDMP"

ORIGIN

Query Match 99.6%; Score 7510.4; DB 6; Length 7542;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 7529; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

Qy	1	CCGTCTCTGGCGCGGAGCGGGACGATGCTGACCCCTTAGATCCTGCTCCAGCTGCGCCGA	60
Db	1	CCGTCTCTGGCGCGGAGCGGGACGATGCTGACCCCTTAGATCCTGCTCCAGCTGCGCCGA	60
Qy	61	GGGAAGAGGGGGCGCCCTCCCCGACCCCGCCCTCCATCGGGTGGCCCTTTTTTTTC	120
Db	61	GGGAAGAGGGGGCGCCCTCCCCGACCCCGCCCTCCATCGGGTGGCCCTTTTTTTTC	120
Qy	121	TCTTCCTCTCGGGGGCTGCTTCGCCGAAGGTAGCGCTGTACGGGCAACCGGAGCCTGG	180
Db	121	TCTTCCTCTCGGGGGCTGCTTCGCCGAAGGTAGCGCTGTACGGGCAACCGGAGCCTGG	180
Qy	181	GCGCGAACGAAGAAGCCGGAACAAAGTGAGGGGAAGCCCGCGCTAGTCGGGGAGCCCC	240
Db	181	GCGCGAACGAAGAAGCCGGAACAAAGTGAGGGGAAGCCCGCGCTAGTCGGGGAGCCCC	240
Qy	241	CGGGAACCCAGGGGAAGCGGGACTCTACGCCAGGCGGGCTTCCCTGAGACCCGGCGCCC	300
Db	241	CGGGAACCCAGGGGAAGCGGGACTCTACGCCAGGCGGGCTTCCCTGAGACCCGGCGCCC	300

Qy	301	CGCGGGCAGCATGCCCTGAGGGCAGGGGGAGCTGAGCTGAACTGGCCCTCCTGGGGACTC	360
Db	301	CGCGGGCAGCATGCCCTGAGGGCAGGGGGAGCTGAGCTGAACTGGCCCTCCTGGGGACTC	360
Qy	361	AGCAAGCTCTCTAGAGCCCCCACATGCTCCCCACCGGGTCCCCGTTGCGTGAGGACA	420
Db	361	AGCAAGCTCTCTAGAGCCCCCACATGCTCCCCACCGGGTCCCCGTTGCGTGAGGACA	420
Qy	421	CCTCCTCTGAGGGGCTCCGCTCGCCCCCTCTTCGGACCCCCCGGGGCCCGGTGGCCAGA	480
Db	421	CCTCCTCTGAGGGGCTCCGCTCGCCCCCTCTTCGGACCCCCCGGGGCCCGGTGGCCAGA	480
Qy	481	GGATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCA	540
Db	481	GGATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCA	540
Qy	541	CGCAGCTCAACGACCTGTCCGGGGCCGGGGGC - GGCAGGGGCCGGGTTCGACGAAAAGG	598
Db	541	CGCAGCTCAACGACCTGTCCGGGGCCGGGGGCCGGCAGGGGCCGGGTTCGACGAAAAGG	600
Qy	599	ACCCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGG	658
Db	601	ACCCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGG	660
Qy	659	TTTTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTA	718
Db	661	TTTTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTA	720
Qy	719	ACCCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTA	778
Db	721	ACCCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTA	780
Qy	779	TGTTTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCT	838
Db	781	TGTTTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCT	840
Qy	839	TCGATGACTTCATCTTTGCCTTCTTTGCTGTGGAATGGTGGTGAAGATGGTGGCCTTGG	898
Db	841	TCGATGACTTCATCTTTGCCTTCTTTGCTGTGGAATGGTGGTGAAGATGGTGGCCTTGG	900
Qy	899	GCATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTTCATTG	958
Db	901	GCATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTTCATTG	960
Qy	959	TCATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTGAGCTTCTCCGCAGTCA	1018
Db	961	TCATTGCAGGGATGCTGGAGTATTTCGCTGGACCTGCAGAACGTGAGCTTCTCCGCAGTCA	1020
Qy	1019	GGACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCAGCATGCGCATTC	1078
Db	1021	GGACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCAGCATGCGCATTC	1080
Qy	1079	TCGTACATTACTGCTGGACACCTTGCCATATGCTGGGCAACGTCTGTGCTCTGTTTCT	1138
Db	1081	TCGTACATTACTGCTGGACACCTTGCCATATGCTGGGCAACGTCTGTGCTCTGTTTCT	1140
Qy	1139	TCGTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACC	1198
Db	1141	TCGTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACC	1200

Art Unit: 1646

Qy 1199 GGTGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACC 1258
| | | | |
Db 1201 GGTGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACC 1260
| | | | |

Qy 1259 AGACAGAGAATGAGGACGAGAGCCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGA 1318
| | | | |
Db 1261 AGACAGAGAATGAGGACGAGAGCCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGA 1320
| | | | |

Qy 1319 GATCCTGCAGGAGTGTGCCACACTGCGTGGGAAGGCGGTGGTGGCCACCCTGCAGTC 1378
| | | | |
Db 1321 GATCCTGCAGGAGTGTGCCACACTGCGTGGGAAGGCGGTGGTGGCCACCCTGCAGTC 1380
| | | | |

Qy 1379 TGGACTATGAGACCTATAACAGTTCAGCAACACCACCTGTGTCAACTGGAACCAGTACT 1438
| | | | |
Db 1381 TGGACTATGAGACCTATAACAGTTCAGCAACACCACCTGTGTCAACTGGAACCAGTACT 1440
| | | | |

Qy 1439 ATACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACA 1498
| | | | |
Db 1441 ATACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACA 1500
| | | | |

Qy 1499 TTGGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTGACATCA 1558
| | | | |
Db 1501 TTGGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTGACATCA 1560
| | | | |

Qy 1559 TGTACTTCGTAATGGACGCTCACTCCTTCTACAACCTTCATCTACTTCATTCTTCTCATCA 1618
| | | | |
Db 1561 TGTACTTCGTAATGGACGCTCACTCCTTCTACAACCTTCATCTACTTCATTCTTCTCATCA 1620
| | | | |

Qy 1619 TCGTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCG 1678
| | | | |
Db 1621 TCGTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCG 1680
| | | | |

Qy 1679 AGACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGACGATTCTGTCCAATG 1738
| | | | |
Db 1681 AGACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGACGATTCTGTCCAATG 1740
| | | | |

Qy 1739 CTAGCACCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACC 1798
| | | | |
Db 1741 CTAGCACCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACC 1800
| | | | |

Qy 1799 TGGTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCG 1858
| | | | |
Db 1801 TGGTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCG 1860
| | | | |

Qy 1859 TCGGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCAGTG 1918
| | | | |
Db 1861 TCGGGCTGGGCTGCTCAGCAGCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCAGTG 1920
| | | | |

Qy 1919 GCAGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACC 1978
| | | | |
Db 1921 GCAGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACC 1980
| | | | |

Qy 1979 ACCACCATCACCCTACCACCTGGGTAATGGGACGCTCAGAGTTCCTCGGGCCAGCCAG 2038
| | | | |
Db 1981 ACCACCATCACCCTACCACCTGGGTAATGGGACGCTCAGAGTTCCTCGGGCCAGCCAG 2040
| | | | |

Qy 2039 AGATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACAC 2098
| | | | |
Db 2041 AGATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACAC 2100
| | | | |

Art Unit: 1646

Qy 2099 CCACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTG 2158
|||
Db 2101 CCACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTG 2160

Qy 2159 ACTGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCAT 2218
|||
Db 2161 ACTGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCAT 2220

Qy 2219 CTGGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAG 2278
|||
Db 2221 CTGGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAG 2280

Qy 2279 AGATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCAGCCCTGGGCCCCCACCCTCA 2338
|||
Db 2281 AGATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCAGCCCTGGGCCCCCACCCTCA 2340

Qy 2339 CCAGCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGA 2398
|||
Db 2341 CCAGCTTCAACATCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGA 2400

Qy 2399 GTACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTG 2458
|||
Db 2401 GTACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTG 2460

Qy 2459 GAGCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGT 2518
|||
Db 2461 GAGCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGT 2520

Qy 2519 CCGCTGACCATGTCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACG 2578
|||
Db 2521 CCGCTGACCATGTCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACG 2580

Qy 2579 CTCAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGAGCCTGGGCCCAG 2638
|||
Db 2581 CTCAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGAGCCTGGGCCCAG 2640

Qy 2639 ATGCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGA 2698
|||
Db 2641 ATGCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGA 2700

Qy 2699 TCGTAGATAGCAAATACTTTGGCCGGGAATCATGATCGCCATCCTGGTCAATACACTCA 2758
|||
Db 2701 TCGTAGATAGCAAATACTTTGGCCGGGAATCATGATCGCCATCCTGGTCAATACACTCA 2760

Qy 2759 GCATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCA 2818
|||
Db 2761 GCATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCA 2820

Qy 2819 ACATCGTCTTCACCAGCCTCTTCGCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTC 2878
|||
Db 2821 ACATCGTCTTCACCAGCCTCTTCGCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTC 2880

Qy 2879 CCTTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTGATTGTGGTCATCAGTG 2938
|||
Db 2881 CCTTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTGATTGTGGTCATCAGTG 2940

Qy 2939 TGTGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGA 2998
|||
Db 2941 TGTGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGA 3000

Art Unit: 1646

Qy	2999	TGCGGGTGCTGAAGCTGGTGCGCTTCCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGTCTCA	3058
Db	3001	TGCGGGTGCTGAAGCTGGTGCGCTTCCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGTCTCA	3060
Qy	3059	TGAAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTTCATCTTTCATCT	3118
Db	3061	TGAAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTTCATCTTTCATCT	3120
Qy	3119	TCAGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACA	3178
Db	3121	TCAGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACA	3180
Qy	3179	CGTTGCCAGACCGGAAGAATTTGCACTCCCTGCTCTGGGCCATCGTCACTGTCTTTTCAGA	3238
Db	3181	CGTTGCCAGACCGGAAGAATTTGCACTCCCTGCTCTGGGCCATCGTCACTGTCTTTTCAGA	3240
Qy	3239	TTCTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTT	3298
Db	3241	TTCTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTT	3300
Qy	3299	GGGCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGC	3358
Db	3301	GGGCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGC	3360
Qy	3359	TGGTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAG	3418
Db	3361	TGGTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAG	3420
Qy	3419	AGCCTGATTTCTTTTCGCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCC	3478
Db	3421	AGCCTGATTTCTTTTCGCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCC	3480
Qy	3479	TGGTGGCTTTGGGAGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCC	3538
Db	3481	TGGTGGCTTTGGGAGAACACGCGGAACACGAAAGAGCCTTTTGCCACCCCTCATCATCC	3540
Qy	3539	ATACGGCTGCGACACCAATGTACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCAC	3598
Db	3541	ATACGGCTGCGACACCAATGTACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCAC	3600
Qy	3599	TGGGCTCTGGCTCTCGACGTACAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACC	3658
Db	3601	TGGGCTCTGGCTCTCGACGTACAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACC	3660
Qy	3659	ATGAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAA	3718
Db	3661	ATGAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAA	3720
Qy	3719	GCAGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGGCCCCAGCCTAAAGC	3778
Db	3721	GCAGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGGCCCCAGCCTAAAGC	3780
Qy	3779	GGAGGAGCCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGG	3838
Db	3781	GGAGGAGCCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGG	3840
Qy	3839	ATGAGGAGGAAAGTTTCAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACA	3898
Db	3841	ATGAGGAGGAAAGTTTCAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACA	3900

Art Unit: 1646

Qy 3899 GGGGTTCCCTTGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGC 3958
|||
Db 3901 GGGGTTCCCTTGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGC 3960
Qy 3959 CGGGGCTGCACCGCACAGCCAGCGGCCGAGCTCTGCCTCTGAGCACCAAGACTGTAATG 4018
|||
Db 3961 CGGGGCTGCACCGCACAGCCAGCGGCCGAGCTCTGCCTCTGAGCACCAAGACTGTAATG 4020
Qy 4019 GCAAGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCCAACTGGATG 4078
|||
Db 4021 GCAAGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCCAACTGGATG 4080
Qy 4079 GGGATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCA 4138
|||
Db 4081 GGGATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCA 4140
Qy 4139 GATCCCGGCTTCTGCCTGTTGCCGAGAGCGAGATTCTGGTCGGCCTATATCTTTCTC 4198
|||
Db 4141 GATCCCGGCTTCTGCCTGTTGCCGAGAGCGAGATTCTGGTCGGCCTATATCTTTCTC 4200
Qy 4199 CTCAGTCAAGGTTTCGTCTCCTGTGTACCGGATCATCACCCACAAGATGTTTGACCATG 4258
|||
Db 4201 CTCAGTCAAGGTTTCGTCTCCTGTGTACCGGATCATCACCCACAAGATGTTTGACCATG 4260
Qy 4259 TGGTCCTCGTCATCATCTTCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATG 4318
|||
Db 4261 TGGTCCTCGTCATCATCTTCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATG 4320
Qy 4319 ACCCCACACGCGCTGAGCGCATCTTCTGACCCTCTCCAACCTACATCTTCACGGCAGTCT 4378
|||
Db 4321 ACCCCACACGCGCTGAGCGCATCTTCTGACCCTCTCCAACCTACATCTTCACGGCAGTCT 4380
Qy 4379 TTCTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCT 4438
|||
Db 4381 TTCTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCT 4440
Qy 4439 ACCTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTATCGACA 4498
|||
Db 4441 ACCTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTATCGACA 4500
Qy 4499 TCCTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGC 4558
|||
Db 4501 TCCTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGC 4560
Qy 4559 GGCTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCAGGGACTGAAGCTGG 4618
|||
Db 4561 GGCTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCAGGGACTGAAGCTGG 4620
Qy 4619 TGGTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTG 4678
|||
Db 4621 TGGTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTG 4680
Qy 4679 CCTTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGT 4738
|||
Db 4681 CCTTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGT 4740
Qy 4739 GTCAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGTACC 4798
|||

Art Unit: 1646

Db 4741 GTCAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACC 4800

Qy 4799 GATGGGTCCGGCACAACTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTG 4858
|||||

Db 4801 GATGGGTCCGGCACAACTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTG 4860

Qy 4859 TGCTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTG 4918
|||||

Db 4861 TGCTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTG 4920

Qy 4919 TGGATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCC 4978
|||||

Db 4921 TGGATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCC 4980

Qy 4979 TCCTCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCC 5038
|||||

Db 4981 TCCTCATCGTGGCCTTCTTTGTCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCC 5040

Qy 5039 ATAAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTAC 5098
|||||

Db 5041 ATAAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTAC 5100

Qy 5099 GGAGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGAAGCCCAGTGCAAGC 5158
|||||

Db 5101 GGAGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGAAGCCCAGTGCAAGC 5160

Qy 5159 CCTACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACT 5218
|||||

Db 5161 CCTACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACT 5220

Qy 5219 ACCTGGACCTCTTCATCACTGGTGTATCGGGCTGAACGTGGTCACTATGGCCATGGAAC 5278
|||||

Db 5221 ACCTGGACCTCTTCATCACTGGTGTATCGGGCTGAACGTGGTCACTATGGCCATGGAAC 5280

Qy 5279 ATTACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCG 5338
|||||

Db 5281 ATTACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCG 5340

Qy 5339 TCATCTTTGTCTTTGAGTCAGTTTTCAAACCTTGTGGCCTTTGCGTTCCGCCGTTTCTTCC 5398
|||||

Db 5341 TCATCTTTGTCTTTGAGTCAGTTTTCAAACCTTGTGGCCTTTGGCTTCCGCCGTTTCTTCC 5400

Qy 5399 AGGACAGGTGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACAC 5458
|||||

Db 5401 AGGACAGGTGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACAC 5460

Qy 5459 TGGAGGAGATTGAGGTCAATCTGTCGCTGCCCATCAACCCACCATCATCCGTATCATGA 5518
|||||

Db 5461 TGGAGGAGATTGAGGTCAATCTGTCGCTGCCCATCAACCCACCATCATCCGTATCATGA 5520

Qy 5519 GGGTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCAC 5578
|||||

Db 5521 GGGTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCAC 5580

Qy 5579 TGCTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGT 5638
|||||

Db 5581 TGCTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGT 5640

Qy 5639 TATTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATG 5698
|||||

Art Unit: 1646

Db 5641 TATTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATG 5700

Qy 5699 AGACACACCCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACTTTGGTATGGCCT 5758
|||||

Db 5701 AGACACACCCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACTTTGGTATGGCCT 5760

Qy 5759 TTCTGACCCTCTTCCGAGTCTCCACTGGTGACAACCTGGAATGGTATTATGAAGGACCCTT 5818
|||||

Db 5761 TTCTGACCCTCTTCCGAGTCTCCACTGGTGACAACCTGGAATGGTATTATGAAGGACACCC 5820

Qy 5819 CCCGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCATCTACTTTG 5878
|||||

Db 5821 TCCGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCATCTACTTTG 5880

Qy 5879 TGTCTTCGTGCTGACGGCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGA 5938
|||||

Db 5881 TGTCTTCGTGCTGACGGCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGA 5940

Qy 5939 AGCACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGG 5998
|||||

Db 5941 AGCACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGG 6000

Qy 5999 AGCTGGAGATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCCTCCTCT 6058
|||||

Db 6001 AGCTGGAGATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCCTCCTCT 6060

Qy 6059 GGCCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCA 6118
|||||

Db 6061 GGCCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCA 6120

Qy 6119 CTGCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACGATGGTACCCACC 6178
|||||

Db 6121 CTGCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACGATGGTACCCACC 6180

Qy 6179 CCGAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTCA 6238
|||||

Db 6181 CCGAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTCA 6240

Qy 6239 GCCGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGA 6298
|||||

Db 6241 GCCGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGA 6300

Qy 6299 GATCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCG 6358
|||||

Db 6301 GATCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCG 6360

Qy 6359 TTCACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATC 6418
|||||

Db 6361 TTCACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATC 6420

Qy 6419 TGCTCCAGCCTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCC 6478
|||||

Db 6421 TGCTCCAGCCTCATGGGGCTCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCC 6480

Qy 6479 GCTCCCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGG 6538
|||||

Db 6481 GCTCCCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGG 6540

Qy 6539 ATGTGCAGGGCCTGGGTAGCCGGAAGACCTGTTGTGTCAGAGGTGAGTGGGCCCTCTGCC 6598
|||||

Art Unit: 1646

Db 6541 ATGTGCAGGGCCTGGGTAGCCGGAAGACCTGTTGTCTCAGAGGTGAGTGGGCCCTCCTGCC 6600

Qy 6599 CTCTGACCCGGTCCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCG 6658
|||||

Db 6601 CTCTGACCCGGTCCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCG 6660

Qy 6659 GCATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAAC 6718
|||||

Db 6661 GCATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAAC 6720

Qy 6719 CCAGCTGGGCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGA 6778
|||||

Db 6721 CCAGCTGGGCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGA 6780

Qy 6779 GCTGGATTTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCTGTTCCACGGGACC 6838
|||||

Db 6781 GCTGGATTTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCTGTTCCACGGGACC 6840

Qy 6839 TGAAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAG 6898
|||||

Db 6841 TGAAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAG 6900

Qy 6899 ATGAACAGCGGAGACACTCCATTGCTGTCTGCTGTCTGGACAGCGGCTCCCAACCCGCC 6958
|||||

Db 6901 ATGAACAGCGGAGACACTCCATTGCTGTCTGCTGTCTGGACAGCGGCTCCCAACCCGCC 6960

Qy 6959 TATGTCCAAGCCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCTGGGAGCCGGCCTA 7018
|||||

Db 6961 TATGTCCAAGCCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCTGGGAGCCGGCCTA 7020

Qy 7019 AGAAAAAACTCAGCCACCCAGTATCTCTATAGACCCCCCGAGAGCCAGGGCTCTCGGC 7078
|||||

Db 7021 AGAAAAAACTCAGCCACCCAGTATCTCTATAGACCCCCCGAGAGCCAGGGCTCTCGGC 7080

Qy 7079 CCCCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATC 7138
|||||

Db 7081 CCCCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATC 7140

Qy 7139 CCTCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCTCCCCAAAGAAAGACACGC 7198
|||||

Db 7141 CCTCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCTCCCCAAAGAAAGACACGC 7200

Qy 7199 TGAGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCCTGAGTCCTACCCACTC 7258
|||||

Db 7201 TGAGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCCTGAGTCCTACCCACTC 7260

Qy 7259 TCCCCCATCACCTTTCTCCACCGGGTGACAGATCCTACGTCCGCCTCCTGGGCAGCGTTTC 7318
|||||

Db 7261 TCCCCCATCACCTTTCTCCACCGGGTGACAGATCCTACGTCCGCCTCCTGGGCAGCGTTTC 7320

Qy 7319 TGAAAAGTCCACGTAAGCAGCAAGCAGCCACGAGGCACCTCACCTGCCTTCTTCAGTGG 7378
|||||

Db 7321 TGAAAAGTCCACGTAAGCAGCAAGCAGCCACGAGGCACCTCACCTGCCTTCTTCAGTGG 7380

Qy 7379 CTGGTGGGGATGACGAGCAGAACTTCCGGAGAGTCGATCTGAAGAGAACACAGCCCTGGA 7438
|||||

Db 7381 CTGGTGGGGATGACGAGCAGAACTTCCGGAGAGTCGATCTGAAGAGAACACAGCCCTGGA 7440

Qy 7439 GCCCCTGCCTCCGGAAGAAGGAAAAGGAGAAGCCAGTGTGGCCAAGGCTCCCGACACC 7498
|||||

Art Unit: 1646

```
Db      7441  GCCCCTGCCTCCGGGAAGAAGGAAAAGGAGAAGCCCAGTGTGGCCAAGGCTCCCGACACC 7500
Qy      7499  AGGAGCTGTTGGGAGAAGCAATACGTTTGTGCAGAATCTCTA 7540
          |||||||||||||||||||||||||||||||||||||||
Db      7501  AGGAGCTGTTGGGAGAAGCAATACGTTTGTGCAGAATCTCTA 7542
```

Run on: February 9, 2007, 00:44:55 ; Search time 67 Seconds
(without alignments)
3284.295 Million cell updates/sec

Title: US-09-346-794-24
Perfect score: 12028
Sequence: 1 MLPHRVPRCVRTPPLRGSAR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Art Unit: 1646

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	11657	96.9	2254	2	T09053	low voltage-activa
2	3553	29.5	1657	2	T15838	hypothetical prote
3	1720.5	14.3	1810	2	T31092	probable voltage-g
4	1676	13.9	2339	2	A42566	omega-conotoxin-se
5	1665.5	13.8	2259	2	S29236	calcium channel pr
6	1653.5	13.7	2272	2	C54972	voltage-dependent
7	1652.5	13.7	1891	2	T43262	calcium channel al
8	1652.5	13.7	2178	2	S29237	calcium channel pr
9	1650.5	13.7	2288	2	S41080	calcium channel al
10	1642	13.7	2223	2	A47447	calcium channel pr
11	1640.5	13.6	2237	2	T45115	N-type calcium cha
12	1638	13.6	2251	2	B54972	voltage-dependent
13	1637.5	13.6	2270	2	A54972	voltage-dependent
14	1636	13.6	1993	2	T30902	sodium channel SCA
15	1632.5	13.6	2222	2	A37490	voltage-dependent
16	1632.5	13.6	2336	2	A45386	omega-conotoxin-se
17	1631	13.6	2181	2	A38198	calcium channel al
18	1628	13.5	1873	2	A30063	dihydropyridine re
19	1622	13.5	2161	2	JH0564	calcium channel al
20	1619.5	13.5	1911	2	T43048	calcium channel al
21	1616	13.4	1852	2	A37860	calcium channel pr
22	1614.5	13.4	1977	2	S54771	sodium channel alp
23	1613	13.4	2203	2	T42742	voltage-dependent
24	1610	13.4	2143	2	JH0427	voltage-dependent
25	1603	13.3	1610	2	A46227	voltage-dependent
26	1595.5	13.3	1783	2	T37258	probable voltage-d
27	1595	13.3	2166	2	S11339	calcium channel pr
28	1592.5	13.2	2139	2	A44467	voltage-dependent
29	1587.5	13.2	1646	2	JH0422	voltage-dependent
30	1587.5	13.2	1873	2	A55645	calcium channel, v
31	1585.5	13.2	2016	2	A38195	sodium channel pro
32	1580	13.1	1917	2	C88728	protein C48A7.1 [i
33	1577.5	13.1	1559	2	T30535	calcium channel al
34	1574	13.1	2171	2	S05054	calcium channel al
35	1573	13.1	2108	2	S72458	sodium channel pro
36	1567.5	13.0	1687	2	S41742	calcium channel al
37	1565	13.0	1957	2	S68453	sodium channel pro
38	1557.5	12.9	2220	2	A45290	calcium channel pr
39	1556	12.9	2019	2	A33996	sodium channel pro
40	1551.5	12.9	1840	1	CHRTM1	sodium channel pro
41	1549	12.9	1976	2	I56555	sodium channel pro
42	1546.5	12.9	1983	2	A60054	sodium channel pro
43	1546	12.9	2262	2	T30890	calcium channel al
44	1544.5	12.8	1951	2	S00320	sodium channel pro
45	1544.5	12.8	2005	2	A46269	sodium channel alp

ALIGNMENTS

RESULT 1

T09053

low voltage-activated, T-type calcium channel alpha chain - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

Art Unit: 1646

C;Accession: T09053
R;Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.; Fox, M.; Rees, M.; Lee, J.H.
Nature 391, 896, 1998
A;Title: Molecular characterization of a neuronal low voltage-activated, T-type, calcium channel.
A;Reference number: Z16538; MUID:98154730; PMID:9495342
A;Accession: T09053
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2254
A;Cross-references: UNIPROT:O54898; UNIPARC:UPI00000009B4; EMBL:AF027984; NID:g3786350; PIDN:AAC67372.1; PID:g3786351
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Map position: 17
A;Note: CACNA1G
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: calcium channel; voltage-gated ion channel

Query Match 96.9%; Score 11657; DB 2; Length 2254;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2219; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	62	GAAGAGSTEKDPGSADSEAAGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERSM	121
Db	30	GRQGPSTEKDPGSADSEAAGLPYPALAPVVFYLSQDSRPRSWCLRTVCNPWFERSM	89
Qy	122	VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG	181
Db	90	VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG	149
Qy	182	DTWNRLDFFIIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVLTLLDITLP	241
Db	150	DTWNRLDFFIIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVLTLLDITLP	209
Qy	242	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQYQTENEDESPF	301
Db	210	MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYQYQTENEDESPF	269
Qy	302	ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNC SAGEHN	361
Db	270	ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNC SAGEHN	329
Qy	362	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL	421
Db	330	PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL	389
Qy	422	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIYLKRAAR	481
Db	390	CLVVIATQFSETKQRESQLMREQVRFLSNASTLASFSEPGSCYEELLKYLVIYLKRAAR	449
Qy	482	RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSTRSHRRLSVHHLVHHHHHHHHHHYHLGN	541
Db	450	RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSTRSHRRLSVHHLVHHHHHHHHHHYHLGN	509
Qy	542	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ	601
Db	510	GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ	569

Qy	602	APPPRCPEASGRTVSGKVPYPTVHTSPPEILKDKALVEVAPSPGPPTLTFSNIIPPGPF	661
Db	570	APPPRCPEASGRTVSGKVPYPTVHTSPPEILKDKALVEVAPSPGPPTLTFSNIIPPGPF	629
Qy	662	SSMHKLELTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD	721
Db	630	SSMHKLELTQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD	689
Qy	722	SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG	781
Db	690	SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAPSSVLAFWRLICDTFRKIVDSKYFGRG	749
Qy	782	IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVYGPFGYIKNPYN	841
Db	750	IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLVLVYGPFGYIKNPYN	809
Qy	842	IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFPLALQRLVVLMTMDNVATF	901
Db	810	IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFPLALQRLVVLMTMDNVATF	869
Qy	902	CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTVFQILTQEDWNKV	961
Db	870	CMLLMFLFIFISILGMHLFGCKFASERDGTLPDRKNFDSLLWAIIVTVFQILTQEDWNKV	929
Qy	962	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDDFFSPSVD	1021
Db	930	LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDDFFSPSVD	989
Qy	1022	GDGDRKKRLALVALGEHAELRKSLPLLIHTAATPMShPKSSSTGVGEALGSGSRRTSS	1081
Db	990	GDGDRKKRLALVALGEHAELRKSLPLLIHTAATPMShPKSSSTGVGEALGSGSRRTSS	1049
Qy	1082	SGSAEPGAHHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS	1141
Db	1050	SGSAEPGAHHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS	1109
Qy	1142	LLSGEGQESQDEEESSEEDRASPAAGSDHRHRSGLEREAKSSFDPDLQVPGLHRTASGR	1201
Db	1110	LLSGEGQESQDEEESSEEDRASPAAGSDHRHRSGLEREAKSSFDPDLQVPGLHRTASGR	1169
Qy	1202	SSASEHQDCNGKSASGRLARTLRDTPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRE	1261
Db	1170	SSASEHQDCNGKSASGRLARTLRDTPQLDGGDDNDEGNLSKGERIQAWVRSRLPACCRE	1229
Qy	1262	RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFL	1321
Db	1230	RDSWSAYIFPPQSRFRLLCHRIITHKMFHDHVLVLIIFLNCITIAMERPKIDPHSAERIFL	1289
Qy	1322	TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG	1381
Db	1290	TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG	1349
Qy	1382	TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICAFFIIFGILG	1441
Db	1350	TKILGMLRVLRLRLTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICAFFIIFGILG	1409
Qy	1442	VQLFKGKFFVCQGEDTRNITNKSDCAEASRYRWRHKYNFDNLGQALMSLFVLASKDGWVD	1501
Db	1410	VQLFKGKFFVCQGEDTRNITNKSDCAEASRYRWRHKYNFDNLGQALMSLFVLASKDGWVD	1469

Art Unit: 1646

Qy	1502	IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE	1561
Db	1470	IMYDGLDAVGVDQQPIMNHNPMWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE	1529
Qy	1562	EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSYDSRFRLLVHHLCTSHYLDLFTITGVI	1621
Db	1530	EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSYDSRFRLLVHHLCTSHYLDLFTITGVI	1589
Qy	1622	GLNVVTMAMEHYQQPQILDEALKICNYIFTVI FVFESVFKLVAFARFRFFQDRWNQLDLA	1681
Db	1590	GLNVVTMAMEHYQQPQILDEALKICNYIFTVI FVFESVFKLVAFARFRFFQDRWNQLDLA	1649
Qy	1682	IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLHTVMQALP	1741
Db	1650	IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIRARVLKLLKMAVGMRALLHTVMQALP	1709
Qy	1742	QVGNLGLLFFMLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTFRVSTG	1801
Db	1710	QVGNLGLLFFMLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTFRVSTG	1769
Qy	1802	DNWNGIMKDP SRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA	1861
Db	1770	DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLNVVIAVLMKHLEESNKEA	1829
Qy	1862	KEEAEEAELEEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF	1921
Db	1830	KEEAEEAELEEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF	1889
Qy	1922	SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCNRNGSTAERSLGHRGWGL	1981
Db	1890	SLEHPTMVPHPPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCNRNGSTAERSLGHRGWGL	1949
Qy	1982	PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR	2041
Db	1950	PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR	2009
Qy	2042	RQAAIRTDSDLVDVQGLGSRDILLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI	2101
Db	2010	RQAAIRTDSDLVDVQGLGSRDILLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI	2069
Qy	2102	RLPAPCPGLEPSWAKDPPETRSSLLELDTLSWISGDLLPSSQEELFPRDLKKCYSVETQ	2161
Db	2070	RLPAPCPGLEPSWAKDPPETRSSLLELDTLSWISGDLLPSSQEELFPRDLKKCYSVETQ	2129
Qy	2162	SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGQPLGGPGSRPKKLSPPSIS	2221
Db	2130	SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGQPLGGPGSRPKKLSPPSIS	2189
Qy	2222	IDPPESQGSRPCCSPGVCLRRRAPASDSKDPVS S S P L D S T A A S P S P K K D T L S L S G L S S D P	2281
Db	2190	IDPPESQGSRPCCSPGVCLRRRAPASDSKDPVS S S P L D S T A A S P S P K K D T L S L S G L S S D P	2249
Qy	2282	TDMDP 2286	
Db	2250	TDMDP 2254	